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(21) International Application Number: PCT/US99/07417 (22) International Filing Date: 2 April 1999 (02.04.99) (30) Priority Data: 09/060,939 15 April 1998 (15.04.98) US (71) Applicant: GENENTECH, INC. [US/US]; 1 DNA Way, South San Francisco, CA 94080-4990 (US). (72) Inventors: DE SAUVAGE, Frederic, J.; 187 Shooting Star Isle, Foster City, CA 94404 (US). CARPENTER, David, A.; 1582 22nd Avenue, San Francisco, CA 94122 (US). (74) Agents: SVOBODA, Craig, G. et al.; Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080-4990 (US).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i>
(54) Title: VERTEBRATE PATCHED-2 PROTEIN (57) Abstract The present invention relates to nucleotide sequences, including expressed sequence tags (ESTs), oligonucleotide probes, polypeptides, antibodies, vectors and host cells expressing, immunoadhesins, agonists and antagonists to <i>patched-2</i> .		

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VERTEBRATE PATCHED-2 PROTEIN

FIELD OF THE INVENTION

5 The present invention relates generally to signaling molecules, specifically to signaling and mediator molecules in the hedgehog (*hh*) cascade which are involved in cell proliferation and differentiation.

BACKGROUND OF THE INVENTION

10 Development of multicellular organisms depends, at least in part, on mechanisms which specify, direct or maintain positional information to pattern cells, tissues, or organs. Various secreted signaling molecules, such as members of the transforming growth factor-beta (TGF- β), Wnt, fibroblast growth factors and hedgehog families have been associated with patterning activity of different cells and structures in *Drosophila* as well as in vertebrates. Perrimon, *Cell*: 80: 517-520 (1995).

15 Segment polarity genes were first discovered in *Drosophila*, which when mutated caused a change in the pattern of structures of the body segments. These changes affected the pattern along the head to tail axis. Hedgehog (*Hh*) was first identified as a segment-polarity gene by a genetic screen in *Drosophila melanogaster*, Nusslein-Volhard *et al.*, *Roux. Arch. Dev. Biol.* 193: 267-282 (1984), that plays a wide variety of developmental functions. Perrimon, *supra*. Although only one *Drosophila Hh* gene has been identified, three mammalian *Hh* homologues have been isolated: Sonic *Hh* (*Shh*), Desert *Hh* (*Dhh*) and Indian *Hh* (*Ihh*), Echelard *et al.*, *Cell* 75: 1417-30 (1993); Riddle *et al.*, *Cell* 75: 1401-16 (1993). *Shh* is expressed at high
20 level in the notochord and floor plate of developing vertebrate embryos, and acts to establish cell fate in the developing limb, somites and neural tube. *In vitro* explant assays as well as ectopic expression of *Shh* in transgenic animals show that *SHh* plays a key role in neural tube patterning, Echelard *et al.* (1993), *supra*; Ericson *et al.*, *Cell* 81: 747-56 (1995); Marti *et al.*, *Nature* 375: 322-5 (1995); Roelink *et al.* (1995), *supra*; Hynes *et al.*, *Neuron* 19: 15-26 (1997). *Hh* also plays a role in the development of limbs (Krauss *et al.*, *Cell*
25 75: 1431-44 (1993); Laufer *et al.*, *Cell* 79, 993-1003 (1994)), somites (Fan and Tessier-Lavigne, *Cell* 79, 1175-86 (1994); Johnson *et al.*, *Cell* 79: 1165-73 (1994)), lungs (Bellusci *et al.*, *Develop.* 124: 53-63 (1997) and skin (Oro *et al.*, *Science* 276: 817-21 (1997)). Likewise, *Ihh* and *Dhh* are involved in bone, gut and germinal cell development, Apelqvist *et al.*, *Curr. Biol.* 7: 801-4 (1997); Bellusci *et al.*, *Development* 124: 53-63 (1997); Bitgood *et al.*, *Curr. Biol.* 6: 298-304 (1996); Roberts *et al.*, *Development* 121: 3163-74
30 (1995). Specifically, *Ihh* has been implicated in chondrocyte development [Vortkamp, A. *et al.*, *Science* 273: 613-22 (1996)] while *Dhh* plays a key role in testis development. Bitgood *et al.*, *supra*. With the exception of the gut, in which both *Ihh* and *Shh* are expressed, the expression patterns of the hedgehog family members do not overlap. Bitgood *et al.*, *supra*.

35 At the cell surface, *Hh* function appears to be mediated by a multicomponent receptor complex involving patched (*ptch*) and smoothened (*smo*), two multi-transmembrane proteins initially identified as segment polarity genes in *Drosophila* and later characterized in vertebrates. Nakano *et al.*, *Nature* 341: 508-513 (1989); Goodrich *et al.*, *Genes Dev.* 10: 301-312 (1996); Marigo *et al.*, *Develop.* 122: 1225-1233 (1996); van den Heuvel, M. & Ingham, P.W., *Nature* 382: 547-551 (1996); Alcedo, J. *et al.*, *Cell* 86: 221-232 (1996); Stone, D.M. *et al.*, *Nature* 384: 129-34 (1996). Upon binding of *Hh* to *Ptch*, the normal inhibitory
40 effect of *Ptch* on *Smo* is relieved, allowing *Smo* to transduce the *Hh* signal across the plasma membrane. It

remains to be established if the *Ptch/Smo* receptor complex mediates the action of all 3 mammalian hedgehogs or if specific components exist. Interestingly, a second murine *Ptch* gene, *Ptch-2* was recently isolated [Motoyama, J. *et al.*, *Nature Genetics* 18: 104-106 (1998)], but its function as a *Hh* receptor has not been established. In order to characterize *Ptch-2* and compare it to *Ptch* with respect to the biological function of the various *Hh* family members, Applicants have isolated the human *Ptch-2* gene. Biochemical analysis of *Ptch* and *Ptch-2* show that both bind to all members of the *Hh* family with similar affinity and that both molecules can form a complex with *Smo*. However, the expression patterns of *Ptch-2* and *Ptch* do not overlap. While *Ptch* is expressed throughout the mouse embryo, *Ptch-2* is found mainly in spermatocytes which require Desert Hedgehog (*Dhh*) for proper development suggesting that *Ptch-2* mediates *Dhh*'s activity in the testis. Chromosomal localization of *Ptch-2* places it on chromosome 1p33-34, a region deleted in some germ cell tumors, raising the possibility that *Ptch-2* may be a tumor suppressor in *Dhh* target cells.

SUMMARY OF THE INVENTION

In one embodiment, the invention provides an isolated nucleic acid molecule having at least about 80% sequence identity to (a) a DNA molecule encoding a patched-2 polypeptide comprising the sequence of amino acids 1 to 1203 of Fig. 1, or (b) the complement of the DNA molecule of (a); and encoding a polypeptide having *patched-2* biological activity. The sequence identity preferably is > 91%, more preferably about 92%, most preferably about 95%. In one aspect, the isolated nucleic acid has at least > 91%, preferably at least about 92%, and even more preferably at least about 95% sequence identity with a polypeptide having amino acid residues 1 to about 1203 of Fig. 1. In a further aspect, the isolated nucleic acid molecule comprises DNA encoding a human *patched-2* polypeptide having amino acid residues 1 to about 1203 of Fig. 1. In yet another aspect, the invention provides for an isolated nucleic acid comprising DNA having at least a 95% sequence identity to (a) a DNA molecule encoding the same mature polypeptide encoded by the cDNA in ATCC Deposit No. 209778 (designation: pRK7.hptc2.Flag-1405), alternatively the coding sequence of clone pRK7.hptc2.Flag-1405, deposited under accession number ATCC 209778. In a still further aspect, the invention provides for a nucleic acid comprising human *patched-2* encoding sequence of the cDNA in ATCC deposit No. 209778 (designation: pRK7.hptc2.Flag-1405) or a sequence which hybridizes thereto under stringent conditions.

In another embodiment, the invention provides a vector comprising DNA encoding a human *patched-2* polypeptide. A host cell comprising such a vector is also provided. By way of example, the host cells may be mammalian cells, (e.g. CHO cells), prokaryotic cells (e.g., *E. coli*) or yeast cells (e.g., *Saccharomyces cerevisiae*). A process for producing *patched-2* polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of *patched-2* and recovering the same from the cell culture.

In yet another embodiment, the invention provides an isolated *patched-2* polypeptide. In particular, the invention provides isolated native sequence *patched-2* polypeptide, which in one embodiment is a human *patched-2* including an amino acid sequence comprising residues 1 to about 1203 of Figure 1. Human *patched-2* polypeptides with or without the initiating methionine are specifically included. Alternatively, the invention provides a human *patched-2* polypeptide encoded by the nucleic acid deposited under accession

number ATCC Deposit No. 209778.

In yet another embodiment, the invention provides chimeric molecules comprising a *patched-2* polypeptide patched-2 to a heterologous polypeptide or amino acid sequence. An example of such a chimeric molecule comprises a *patched-2* polypeptide patched-2 to an epitope tag sequence or a constant region of an immunoglobulin.

In yet another embodiment, the invention provides expressed sequence tag (EST) comprising the nucleotide sequences identified in Fig. 2A (905531) (SEQ ID NO:3) and Fig. 2B (1326258) (SEQ ID NO:5).

In yet another embodiment, the invention provides for alternatively spliced variants of human *patched-2* having patched-2 biological activity.

In yet another embodiment, the invention provides for method of using *patched-2* for the treatment of disorders which are mediated at least in part by Hedgehog (Hh), especially Desert hedgehog (*Dhh*). In particular, testicular cancer. In yet another embodiment, the invention provides a method of using antagonists or agonists of *patched-2* for treating disorders or creating a desirable physiological condition effected by blocking *Hh* signaling, especially *Dhh* signaling. (E.g. contraception).

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the nucleotide (SEQ ID NO:1) and derived amino acid (SEQ ID NO:2) sequence of a native sequence of human *Ptch-2*.

Figure 2A shows EST 905531 (SEQ ID NO:3) and Fig. 2B shows EST 1326258 (SEQ ID NO:5) in alignment with human *Ptch* (SEQ ID NO:18). These ESTs were used in the cloning of human full-length *Ptch-2* (SEQ ID NO:1).

Figure 3 shows a comparison between human *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2). Gaps introduced for optimal alignment are indicated by dashes. Identical amino acids are boxed. The 12 transmembrane domains are indicated by the gray boxes, all of which are conserved between the two sequences. Alignment results between the two sequences indicate 53% identity. The most significant difference is a shorter C-terminal intracellular domain in human *Ptch-2* (SEQ ID NO:2) in comparison with human *Ptch* (SEQ ID NO:4).

Figure 4 shows a northern blot of *Ptch-2* (SEQ ID NO:2) which indicates expression is limited to the testis. Multiple human fetal and adult tissue northern blots were probed with fragments corresponding to the 3'-untranslated region of murine *Ptch-2*.

Figure 5 shows a chromosomal localization of two BAC clones which were isolated by PCR screening with human *patched-2* derived probes. Both probes were mapped by FISH to human chromosome 1p33-34.

Figure 6 is an *in situ* hybridization comparing *Ptch* (SEQ ID NO:4), *Ptch-2* (SEQ ID NO:2) and *Fused* (FuRK) (SEQ ID NO:10) expression. High magnification of mouse testis showing expression of (a) *Ptch*, *Ptch-2* (SEQ ID NO:2) (b) and FuRK (SEQ ID NO:10) (c). Low magnification of testis section hybridized with *Ptch-2* sense (SEQ ID NO:11) (d) and anti-sense probe (SEQ ID NO:12) (e) respectively. Fig. 6(f) shows low magnification of testis section hybridized with FuRK (SEQ ID NO:10 encoding nucleic acid). Scale bar: a, b, c: 0.05 mm; d, e, f: 0.33 mm.

Figure 7A is logarithmic plot comparing the binding *Ptch-2* (SEQ ID NO:2) to *Dhh* (SEQ ID

NO:13) and *Shh* (SEQ ID NO:14). Competitive binding of recombinant murine ^{125}I -*Shh* to 293 cells overexpressing *Ptch* (SEQ ID NO:4) or *Ptch-2* (SEQ ID NO:2). There was no detectable binding to mock transfected cells (data not shown). Figure 7B is a western blot illustrating co-immunoprecipitation of epitope tagged *Ptch* (SEQ ID NO:4) or *Ptch-2* (SEQ ID NO:2) with epitope tagged *Smo* (SEQ ID NO:15).

Immunoprecipitation was performed with antibodies to the Flag tagged *Ptch* (SEQ ID NO:4) and analyzed on a 6% acrylamide gel with antibodies to the Myc tagged *Smo* (SEQ ID NO:15). Protein complexes can be detected for both *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) with *Smo* (SEQ ID NO:15). *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) express at similar levels as shown by immunoprecipitation using antibodies to the Flag-tag and western blot using the same anti-Flag antibody.

Figure 8 is a sequence comparison between human *Ptch-2* (SEQ ID NO:2) and murine *Ptch-2* (SEQ ID NO:7), which indicates that there is about 91% identity between the two sequences.

Figure 9 is an *in situ* hybridization which demonstrates the accumulation of *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) mRNA detected by *in situ* hybridization in basal cells of E18 transgenic mice overexpressing *SMO-M2* (SEQ ID NO:16) (Xie *et al.*, *Nature* 391: 90-92 (1998)).

Figure 10 is a partial sequence representing clone 3A (SEQ ID NO:8), a partial *patched-2* fragment which was initially isolated from a fetal brain library.

Figure 11 is a partial sequence representing clone 16.1 (SEQ ID NO:9), a partial *patched-2* fragment which isolated from a testis library.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

The terms "*patched-2*" and "*patched-2* polypeptide" when used herein encompass native sequence *patched-2* and *patched-2* variants (which are further defined herein) having *patched-2* biological activity. *Patched-2* may be isolated from a variety of sources, such as from testes tissue types or from another source, or prepared by recombinant or synthetic methods.

A "native sequence *patched-2*" comprises a polypeptide having the same amino acid sequence as a human *patched-2* derived from nature. Such native sequence *patched-2* can be isolated from nature or can be produced by recombinant and/or synthetic means. The term "native sequence vertebrate *patched-2*" specifically encompasses naturally occurring truncated forms of human *patched-2*, naturally occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of human *patched-2*. Thus, one embodiment of the invention, the native sequence *patched-2* is a mature or full-length native *Ptch-2* comprising amino acids 1 to 1203 of Fig. 1 (SEQ ID NO:2) with or without the initiating methionine at position 1.

"*Patched-2* variant" means an active human *patched-2* as defined below having at least > 91% amino acid sequence identity to (a) a DNA molecule encoding a *patched-2* polypeptide, or (b) the complement of the DNA molecule of (a). In a particular embodiment, the *patched-2* variant has at least > 91% amino acid sequence homology with the human *Ptch-2* (SEQ ID NO:2) having the deduced amino acid sequence shown in Fig. 1 for a full-length native sequence human *patched-2*. Such *patched-2* variants

include, without limitation, *patched-2* polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the sequence of Fig. 1 (SEQ ID NO:2). Preferably, the nucleic acid or amino acid sequence identity is at least about 92%, more preferably at least about 93%, and even more preferably at least about 95%.

5 "Percent (%) amino acid sequence identity" with respect to the *patched-2* sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the *patched-2* sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid
10 sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST-2 software that are set to their default parameters. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

"Percent (%) nucleic acid sequence identity" with respect to the *patched-2* sequences identified
15 herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the *patched-2* sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST-2 software that are set to their default parameters.
20 Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising *patched-2* polypeptide, or a portion thereof, *patched-2* to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not
25 interfere with activity of the *patched-2* polypeptide. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 to about 50 amino acid residues (preferably, between about 10 to about 20 residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the
30 binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesin comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a
35 ligand. The immunoglobulin constant domain sequence in the immunoadhesins may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3 or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM. Immunoadhesion reported in the literature include fusions of the T cell receptor [Gascoigne *et al.*, *Proc. Natl. Acad. Sci. USA* 84: 2936-2940 (1987)]; CD4* [Capron *et al.*, *Nature* 337: 525-531 (1989); Traunecker *et al.*, *Nature* 339: 68-70 (1989); Zettmeissl *et al.*, *DNA Cell Biol. USA* 9: 347-353 (1990); Byrn

et al., *Nature* 344, 667-670 (1990)); L-selectin (homing receptor) [Watson *et al.*, *J. Cell. Biol.* 110, 2221-2229 (1990); Watson *et al.*, *Nature* 349, 164-167 (1991)]; CD44* [Aruffo *et al.*, *Cell* 61, 1303-1313 (1990)]; CD28* and B7* [Linsley *et al.*, *J. Exp. Med.* 173, 721-730 (1991)]; CTLA-4* [Lisley *et al.*, *J. Exp. Med.* 174, 561-569 (1991)]; CD22* [Stamenkovic *et al.*, *Cell* 66, 1133-1144 (1991)]; TNF receptor [Ashkenazi *et al.*, *Proc. Natl. Acad. Sci. USA* 88, 10535-10539 (1991); Lesslauer *et al.*, *Eur. J. Immunol.* 27, 2883-2886 (1991); Peppel *et al.*, *J. Exp. Med.* 174, 1483-1489 (1991)]; NP receptors [Bennett *et al.*, *J. Biol. Chem.* 266, 23060-23067 (1991)]; IgE receptor α -chain* [Ridgway and Gorman, *J. Cell. Biol.* 115, abstr. 1448 (1991)]; HGF receptor [Mark, M.R. *et al.*, *J. Biol. Chem.*, 267(36): 26166-26171 (1992)], where the asterisk (*) indicates that the receptor is a member of the immunoglobulin superfamily.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends upon the ability of denatured DNA to reanneal when complementary strands are present in an environment near but below their T_m (melting temperature). The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. Moreover, stringency is also inversely proportional to salt concentrations. For additional details and explanation of stringency of hybridization reactions, see Ausubel *et al.*, *Current Protocols in Molecular Biology* (1995).

"Stringent conditions," as defined herein may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (vol/vol) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 μ g/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the vertebrate *patched-2* natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" *patched-2* nucleic acid molecule is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the *patched-2* nucleic acid. An isolated *patched-2* nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated *patched-2* nucleic acid molecules therefore are distinguished from the corresponding native *patched-2* nucleic acid molecule as it exists in natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading frame. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers single monoclonal antibodies (including agonist and antagonist antibodies), antibody compositions with polypeptopic specificity, as well as antibody fragments (e.g., Fab, F(ab')₂ and Fv), so long as they exhibit the desired biological activity.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations that typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they are synthesized by the hybridoma culture, uncontaminated by other immunoglobulins. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by the hybridoma method first described by Kohler & Milstein, *Nature* 256:495 (1975), or may be made by recombinant DNA methods [see, e.g. U.S. Patent No. 4,816,567 (Cabilly *et al.*)].

The monoclonal antibodies herein specifically include "chimeric" antibodies (immunoglobulins) in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while

the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity [U.S. Patent No. 4,816,567; Cabilly *et al.*; Morrison *et al.*, Proc. Natl. Acad. Sci. USA 81, 6851-6855 (1984)].

5 "Humanized" forms of non-human (e.g. murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a
10 non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, corresponding non-human residues replace Fv framework residues of the human immunoglobulin. Furthermore, humanized antibody may comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. These modifications are made to further refine and optimize antibody performance. In general, the humanized antibody will comprise
15 substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details see: Jones *et al.*, Nature 321, 522-525 (1986); Riechmann *et al.*, Nature
20 332, 323-327 (1988); Presta, Curr. Op. Struct. Biol. 2 593-596 (1992) and U.S. Patent No. 5,225,539 (Winter) issued July 6, 1993.

"Active" or "activity" for the purposes herein refers to form(s) of *patched-2* which retain the biologic and/or immunologic activities of native or naturally occurring *patched-2*. A preferred activity is the ability to bind to and affect, e.g., block or otherwise modulate, *hedgehog (Hh)*, especially *desert hedgehog (Dhh)* signaling. For example, the regulation of the pathogenesis of testicular cancer, male spermatocyte
25 formation and basal cell carcinoma.

The term "antagonist" is used herein in the broadest sense to include any molecule which blocks, prevents, inhibits, neutralizes the normal functioning of *patched-2* in the *hedgehog (Hh)* signaling pathway. One particular form of antagonist includes a molecule that interferes with the interaction between *Dhh* and
30 *patched-2*. Alternatively, an antagonist could also be a molecule which increases the levels of *patched-2*. In a similar manner, the term "agonist" is used herein to include any molecule which promotes, enhances or stimulates the binding of a *Hh* to *patched-2* in the *Hh* signaling pathway or otherwise upregulates it (e.g., blocking binding of *Ptch-2* (SEQ ID NO:2) to *Smo* (SEQ ID NO:17). Suitable molecules that affect the protein-protein interaction of *Hh* and *patched-2* and its binding proteins include fragments of the latter or
35 small bioorganic molecules, e.g., peptidomimetics, which will prevent or enhance, as the case may be, the binding of *Hh* to *patched-2*. Non-limiting examples include proteins, peptides, glycoproteins, glycopeptides, glycolipids, polysaccharides, oligosaccharides, nucleic acids, bioorganic molecules, peptidomimetics, pharmacological agents and their metabolites, transcriptional and translation control sequences, and the like.

Another preferred form of antagonist includes antisense oligonucleotides that inhibit proper transcription of wild type *patched-2*.

The term "modulation" or "modulating" means upregulation or downregulation of a signaling pathway. Cellular processes under the control of signal transduction may include, but are not limited to, transcription of specific genes; normal cellular functions, such as metabolism, proliferation, differentiation, adhesion, apoptosis and survival, as well as abnormal processes, such as transformation, blocking of differentiation and metastasis.

The techniques of "polymerase chain reaction," or "PCR", as used herein generally refers to a procedure wherein minute amounts of a specific piece of nucleic acid, RNA and/or DNA are amplified as described in U.S. Pat. No. 4,683,195 issued 28 July 1987. Generally, sequence information from the ends of the region of interest or beyond needs to be available, such that oligonucleotide primers can be designed; these primers will be identical or similar in sequence to opposite strands of the template to be amplified. The 5' terminal nucleotides of the two primers may coincide with the ends of the amplified material. PCR sequences form total genomic DNA, and cDNA transcribed from total cellular RNA, bacteriophage, or plasmid sequences, etc. See generally Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol.* 51: 263 (1987); Erlich, Ed., PCR Technology, (Stockton Press, NY, 1989). As used herein, PCR is considered to be one, but not the only, example of a nucleic acid test sample comprising the use of a known nucleic acid as a primer and a nucleic acid polymerase to amplify or generate a specific piece of nucleic acid.

II. Compositions and Methods of the Invention

A. Full-length *patched-2*

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as *patched-2*. In particular, Applicants have identified and isolated cDNA encoding a human *patched-2* polypeptide, as disclosed in further detail in the Examples below. Using BLAST, BLAST-2 and FastA sequence alignment computer programs (set to the default parameters), Applicants found that a full-length native sequence human *patched-2* (i.e., *Ptch-2* in Figure 3, SEQ ID NO:2) has 53% amino acid sequence identity with a human *patched* (i.e., *Ptch*, SEQ ID NO:4). Moreover a human full-length *patched-2* (i.e., *Ptch-2*, SEQ ID NO:2) has about a 91% sequence identity with murine *Ptch-2* (SEQ ID NO:7) (Fig. 8). Accordingly, it is presently believed that the human *patched-2* (i.e., *Ptch-2*, SEQ ID NO:2) disclosed in the present application is a newly identified member of the mammalian hedgehog signaling cascade, specifically *Desert hedgehog*.

The full-length native sequence of human *patched-2* gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length gene or to isolate still other vertebrate homolog genes (for instance, those encoding naturally-occurring variants of *patched-2* or *patched-2* from other species) which have a desired sequence identity to the human *patched-2* sequence disclosed in Fig.1 (SEQ ID NO:2). Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from the nucleotide sequence of Fig. 1 (SEQ ID NO:1) or from genomic sequences including promoters, enhancer elements and introns of native sequence vertebrate *patched-2*. By way of example, a screening method will comprise isolating the coding region of the vertebrate *patched-2* gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may

be labeled by a variety of labels, including radionucleotides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the vertebrate *patched-2* gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to.

B. Patched-2 Variants

In addition to the full-length native sequence *patched-2* described herein, it is contemplated that *patched-2* variants can be prepared. *Patched-2* variants can be prepared by introducing appropriate nucleotide changes into a known *patched-2* DNA, or by synthesis of the desired *patched-2* polypeptides.

Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of *patched-2*.

Variations in the native full-length sequence *patched-2* or in various domains of the *patched-2* described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the *patched-2* that results in a change in the amino acid sequence of *patched-2* as compared with the native sequence *patched-2*. Optionally, the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of *patched-2*. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the *patched-2* with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity in the *in vitro* assay described in the Examples below.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., *Nucl. Acids Res.*, 13:4331 (1986); Zoller et al., *Nucl. Acids Res.*, 10: 6487 (1987)], cassette mutagenesis [Wells et al., *Gene*, 34:315 (1985)], restriction selection mutagenesis [Wells et al., *Philos. Trans. R. Soc. London SerA*, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the vertebrate *patched-2* variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, *The*

Proteins, (W.H. Freeman & Co., N.Y.): Chothia, *J. Mol. Biol.*, 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

In the comparison between human *patched* and *patched-2* sequences depicted in Figure 3 (e.g., *Ptch*, SEQ ID NO:4 and *Ptch-2*, SEQ ID NO:2), the 12 transmembrane domains are identified in gray, while identical residues are boxed. Gaps are indicated by dashes (-) and are inserted to maximize the total identity score between the two sequences.

C. Modifications of *patched-2*

Covalent modifications of *patched-2* are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of *patched-2* with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the *patched-2*. Derivatization with bifunctional agents is useful, for instance, for crosslinking *patched-2* to a water-insoluble support matrix or surface for use in the method for purifying anti-*patched-2* antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazo-acetyl)-2-phenylethane, glutaraldehyde, N-hydroxy-succinimide esters, for example, esters with 4-azido-salicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis-(succinimidyl-propionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)-dithio]propionimide.

Other modifications include deamidation of glutamyl and asparagyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of *patched-2* comprises linking the *patched-2* polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. Such modifications would be expected to increase the half-life of the molecules in circulation in a mammalian system; Extended half-life of *patched-2* molecules might be useful under certain circumstances, such as where the *patched-2* variant is administered as a therapeutic agent.

The *patched-2* of the present invention may also be modified in a way to form a chimeric molecule comprising *patched-2* bonded to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of *patched-2* with a tag polypeptide, which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the *patched-2*. The presence of such epitope-tagged forms of the *patched-2* can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the *patched-2* to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of the *patched-2* with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Ordinarily, the C-terminus of a contiguous amino acid sequence of a patched-2 receptor is fused to the N-terminus of a contiguous amino acid sequence of an immunoglobulin constant region, in place of the variable region(s). however N-terminal fusions are also possible.

Typically, such fusions retain at least functionally active hinge, CH2 and CH3 domains of the constant region of an immunoglobulin heavy chain. Fusions are also made to the C-terminus of the Fc portion of a constant domain, or immediately N-terminal to the CH1 of the heavy chain or the corresponding region of the light chain. This ordinarily is accomplished by constructing the appropriate DNA sequence and expressing it in recombinant cell culture. Alternatively, immunoadhesins may be synthesized according to known methods.

The precise site at which the fusion is made is not critical; particular sites are well known and may be selected in order to optimize the biological activity, secretion or binding characteristics of the immunoadhesins.

In a preferred embodiment, the C-terminus of a contiguous amino acid sequence which comprises the binding site(s) of *patched-2*, at the N-terminal end, to the C-terminal portion of an antibody (in particular the Fc domain), containing the effector functions of an immunoglobulin, e.g. immunoglobulin G₁ (IgG-1). As herein above mentioned, it is possible to fuse the entire heavy chain constant region to the sequence containing the binding site(s). However, more preferably, a sequence beginning in the hinge region just upstream of the papain cleavage site (which defines IgG Fc chemically; residue 216, taking the first residue of heavy chain constant region to be 114 [Kobayashi *et al.*, *supra*], or analogous sites of other immunoglobulins) is used in the fusion. Although it was earlier thought that in immunoadhesins the immunoglobulin light chain would be required for efficient secretion of the heterologous protein-heavy chain fusion proteins, it has been found that even the immunoadhesins containing the whole IgG1 heavy chain are efficiently secreted in the absence of light chain. Since the light chain is unnecessary, the immunoglobulin heavy chain constant domain sequence used in the construction of the immunoadhesins of the present invention may be devoid of a light chain binding site. This can be achieved by removing or sufficiently altering immunoglobulin heavy chain sequence elements to which the light chain is ordinarily linked so that such binding is no longer possible. Thus, the CH1 domain can be entirely removed in certain embodiments of the *patched-2*/immunoglobulin chimeras.

In a particularly preferred embodiment, the amino acid sequence containing the extracellular domain(s) of *patched-2* is fused to the hinge region and CH2, CH3; or CH1, hinge, CH2 and CH3 domains of an IgG-1, IgG-2, IgG-3, or IgG-4 heavy chain.

In some embodiments, the *patched-2*/immunoglobulin molecules (immunoadhesins) are assembled as monomers, dimers or multimers, and particularly as dimers or tetramers. Generally, these assembled immunoadhesins will have known unit structures similar to those of the corresponding immunoglobulins. A basic four chain structural unit (a dimer of two immunoglobulin heavy chain-light chain pairs) is the form in which IgG, IgA and IgE exist. A four chain unit is repeated in the high molecular weight immunoglobulins; IgM generally exists as a pentamer of basic four-chain units held together by disulfide bonds. IgA globulin, and occasionally IgG globulin, may also exist in a multimeric form in serum. In the case of multimers, each four chain unit may be the same or different.

It is not necessary that the entire immunoglobulin portion of the *patched-2*/immunoglobulin chimeras be from the same immunoglobulin. Various portions of different immunoglobulins may be combined, and

variants and derivatives of native immunoglobulins can be made as herein above described with respect to *patched-2*, in order to optimize the properties of the immunoadhesin molecules. For example, immunoadhesin constructs in which the hinge of IgG-1 was replaced with that of IgG-3 were found to be functional and showed pharmacokinetics comparable to those of immunoadhesins comprising the entire IgG-1 heavy chain.

5 Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8: 2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)]. A preferred tag is the influenza HA tag.

15 D. Preparation of *patched-2*

The description below relates primarily to production of a particular *patched-2* by culturing cells transformed or transfected with a vector containing *patched-2* nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare *patched-2*. For instance, the *patched-2* sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the vertebrate *patched-2* may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length *patched-2*.

1. Isolation of DNA encoding vertebrate *patched-2*

DNA encoding *patched-2* may be obtained from a cDNA library prepared from tissue believed to possess the *patched-2* mRNA and to express it at a detectable level. Accordingly, human *patched-2* DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The vertebrate *patched-2*-encoding gene may also be obtained from a genomic library or by oligonucleotide synthesis.

Libraries can be screened with probes (such as antibodies to the *patched-2* or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding vertebrate *patched-2* is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide

sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ^{32}P -labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook *et al.*, *supra*.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined through sequence alignment using computer software programs such as BLAST, BLAST-2, ALIGN, DNASTar, and INHERIT which employ various algorithms to measure homology.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook *et al.*, *supra*, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for *patched-2* production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in *Mammalian Cell Biotechnology: A Practical Approach*, M. Butler, ed. (IRL Press, 1991) and Sambrook *et al.*, *supra*.

Methods of transfection are known to the ordinarily skilled artisan, for example, CaPO_4 and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook *et al.*, *supra*, or electroporation is generally used for prokaryotes or other cells that contain substantial cell-wall barriers. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw *et al.*, *Gene*, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, *Virology* 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transformations have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen *et al.*, *J. Bact.*, 130:946 (1977) and Hsiao *et al.*, *Proc. Natl. Acad. Sci. (USA)*, 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, *e.g.*, polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown *et al.*, *Methods in Enzymology*, 185:527-537 (1990) and Mansour *et al.*, *Nature*, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote,

yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635).

5 In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for vertebrate *patched-2*-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism.

Suitable host cells for the expression of vertebrate *patched-2* are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as Drosophila S2 and Spodoptera Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham *et al.*, *J. Gen Virol.*, 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, *Biol. Reprod.* 23:243-251 (1980)); human lung cells (WI38, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding *patched-2* may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques, which are known to the skilled artisan.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells. A preferred replicable expression vector is the plasmid pRK5. Holmes *et al.*, *Science*, 253:1278-1280 (1991).

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the *patched-2* nucleic acid, such as DHFR or thymidine kinase.

An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub *et al.*, *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb *et al.*, *Nature*, 282:39 (1979); Kingsman *et al.*, *Gene*, 7:141 (1979); Tschemper *et al.*, *Gene*, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, *Genetics*, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the *patched-2* nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang *et al.*, *Nature*, 275:615 (1978); Goeddel *et al.*, *Nature*, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, *Nucleic Acids Res.*, 8:4057 (1980); EP 36,776], and hybrid promoters such as the *tac* promoter [deBoer *et al.*, *Proc. Natl. Acad. Sci. USA*, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding *patched-2*.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman *et al.*, *J. Biol. Chem.*, 255:2073 (1980)] or other glycolytic enzymes [Hess *et al.*, *J. Adv. Enzyme Reg.*, 7:149 (1968); Holland, *Biochemistry*, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phospho-fructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

Patched-2 transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, *e.g.*, the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Inserting an enhancer sequence into the vector may increase transcription of a DNA encoding the *patched-2* by higher eukaryotes. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at

a position 5' or 3' to the *patched-2* coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding *patched-2*.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of *patched-2* in recombinant vertebrate cell culture are described in Gething *et al.*, *Nature*, 293:620-625 (1981); Mantei *et al.*, *Nature*, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, *Proc. Natl. Acad. Sci. USA*, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence *patched-2* polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence to *patched-2* DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of *patched-2* may be recovered from host cell lysates. Since *patched-2* is membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of *patched-2* can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify *patched-2* from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the *patched-2*. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, *Methods*

in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular *patched-2* produced.

E. Uses for *patched-2*

(1) *Patched-2 is a specific receptor for desert hedgehog (Dhh)*

The *hedgehog (Hh)* signaling pathway has been implicated in the formation of embryonic structures in mammals and invertebrates. The multi-pass transmembrane receptor *patched*, is a negative regulator of the *Hh* pathway, repressing the serpentine signaling molecule *smoothed (Smo)*. Data have shown that loss of *Patched* leads to deregulation of the *Hh* pathway leading to formation of aberrant structures in the embryos and carcinoma in the adult.

Applicants' newly identified second human *patched* gene, termed *patched-2* (e.g., *Pich-2*, SEQ ID NO:2), has a similar 12 transmembrane domain topology as does *patched*, and can bind to all the members of the *Hh* family and can complex with *Smo* (e.g., SEQ ID NO:17). However, the expression patterns of *patched-2* and *patched* do not overlap. *Patched-2* is expressed mainly in the developing spermatocytes, which are supported directly by the *Desert hedgehog* producing Sertoli cells, which suggests that *patched-2* is a receptor for *Desert hedgehog*.

In the adult tubule, Sertoli cells, which are unusually large secretory cells, traverse the seminiferous tubule from the basal lamina to the luminal aspect, sending out cytoplasmic protrusions that engulf the germ cells. These contacts are particularly close during spermiogenesis, in which the haploid round spermatids undergo differentiation to produce the highly specialized, motile sperm. Tight junctions between adjacent Sertoli cells compartmentalize the tubule into a basal region, which contains mitotic spermatogonia and early spermatocytes, and an adluminal compartment, which contains meiotic spermatocytes and maturing spermatids. In fact, a Sertoli-derived cell line supports the meiotic progression of germ cells in culture, consistent with the view that factors derived from Sertoli cells contribute to germ cell maturation, Rassoulzadegan, M., *et al.*, *Cell* 1993, 75: 997-1006. Loss of *Dhh* activity results in a recessive, sex-specific phenotype. Female mice homozygous for the mutation were fully viable and fertile, whereas male mice were viable but infertile. A gross examination indicated that, as early as 18.5 dpc, the testes of mutant males were noticeably smaller than those of heterozygous littermates. Bitgood *et al.*, *Curr. Biol.*, 1996 6(3): 298-304. Thus, Sertoli cells likely independently regulate mitotic and meiotic stages of germ cell development during postnatal development. Therefore, since *patched-2* appears to be the receptor for *Dhh* (SEQ ID NO:13), molecules which modulate the binding of *Dhh* (SEQ ID NO:13) to *patched-2* would affect the activation of *Dhh* (SEQ ID NO:13) signaling, and thereby would have utility in the treatment of conditions which are modulated by *Dhh* (SEQ ID NO:13). (For example, testicular cancer). Alternatively, it is also provided that antagonists or agonists of *patched-2* may be used for treating disorders or creating a desirable physiological condition effected by blocking *Dhh* signaling. (E.g., contraception, infertility treatment).

(2) *General uses for *patched-2**

Nucleotide sequences (or their complement) encoding *patched-2* have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. *Patched-2* nucleic acid will also be useful for the preparation of

patched-2 polypeptides by the recombinant techniques described herein.

The full-length native sequence *patched-2* gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length gene or to isolate still other genes (for instance, those encoding naturally-occurring variants of *patched-2*) which have a desired sequence identity to the *patched-2* sequence disclosed in Fig. 1 (SEQ ID NO:1). Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from the nucleotide sequence of Fig. 1 (SEQ ID NO:1) or from genomic sequences including promoters, enhancer elements and introns of native sequence *patched-2*. By way of example, a screening method will comprise isolating the coding region of the *patched-2* gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ³²P or ³⁵S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the *patched-2* gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine to which members of such libraries the probe hybridizes. Hybridization techniques are described in further detail in the Examples below.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related *patched-2* sequences.

Nucleotide sequences encoding *patched-2* can also be used to construct hybridization probes for mapping the gene, which encodes *patched-2* and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

Patched-2 polypeptides can be used in assays to identify the other proteins or molecules involved in complexing with *patched-2* which ultimately results in the modulation of *hedgehog* signaling. Alternatively, these molecules can modulate the binding of *patched-2* to *Dhh* (SEQ ID NO:13). By such methods, inhibitors of the binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the substrate of *patched-2* can be used to isolate correlative complexing proteins. Screening assays can be designed to find lead compounds that mimic the biological activity of a native *patched-2* or to find those that act as a substrate for *patched-2*. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Such small molecule inhibitors could block the enzymatic action of *patched-2*, and thereby inhibit *hedgehog* signaling. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode *patched-2* or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA sequence that is integrated into the genome of a cell from which a

transgenic animal develops. In one embodiment, cDNA encoding *patched-2* can be used to clone genomic DNA encoding *patched-2* in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding *patched-2*. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for *patched-2* transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding *patched-2* introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding *patched-2*. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression.

Non-human homologues of vertebrate *patched-2* can be used to construct a *patched-2* "knock out" animal which has a defective or altered gene encoding *patched-2* as a result of homologous recombination between the endogenous gene encoding *patched-2* and altered genomic DNA encoding *patched-2* introduced into an embryonic cell of the animal. For example, cDNA encoding *patched-2* can be used to clone genomic DNA encoding *patched-2* in accordance with established techniques. A portion of the genomic DNA encoding *patched-2* can be deleted or replaced with another gene, such as a gene encoding a selectable marker that can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li *et al.*, *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the *patched-2* polypeptide.

Suppression or inhibition (antagonism) of *Dhh* signaling is also an objective of therapeutic strategies. Since *patched-2* can combine with all members of the hedgehog family (i.e., *Shh*, *Dhh*, *Ihh*), antagonist molecules which prevent the binding of hedgehog molecules to *Ptch-2* (SEQ ID NO:2) have therapeutic utility. For example, *SHh* signaling is known to be activated in Basal Cell Carcinoma; *Dhh* (SEQ ID NO:13) is known to be involved in the regulation of spermatogenesis. Inhibitor or antagonist of *Hh* signaling would be effective therapeutics in the treatment of Basal Cell Carcinoma or male contraception, respectively.

The stimulation of *Dhh* signaling (agonism) is also an objective of therapeutic strategies. Since *Ptch-2* (SEQ ID NO:2) also binds to the other members of the *Hh* family, *Ihh* and *Shh*, activating *Dhh* signaling would be useful in disease states or disorders characterized by inactive or insufficient *Hh* signaling.

For example, degenerative disorders of the nervous system, *e.g.*, Parkinson's disease, memory deficits, Alzheimer's disease, Lou Gehrig's disease, Huntington's disease, schizophrenia, stroke and drug addiction. Additionally, *patched-2* agonists could be used to treat gut diseases, bone diseases, skin diseases, diseases of the testis (including infertility), ulcers, lung diseases, diseases of the pancreas, diabetes, osteoporosis.

5 F. Anti-*patched-2* Antibodies

The present invention further provides anti-vertebrate *patched-2* antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

10 The anti-*patched-2* antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the *patched-2* polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the
15 mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants that may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

20 2. Monoclonal Antibodies

The anti-*patched-2* antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of
25 producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the *patched-2* polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes
30 are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that
35 inhibit the growth or survival of the unfused immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression

of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Rockville, Maryland. Human myeloma and mouse-human heteromyeloma cell lines also have been
5 described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against *patched-2*. Preferably, the binding specificity of monoclonal
10 antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution
15 procedures and grown by standard methods [Goding, *supra*]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example,
20 protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are
25 capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be
30 modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison *et al.*, *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-
35 combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another

amin acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Humanized Antibodies

The anti-*patched-2* antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source that is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeven et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)].

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the vertebrate *patched-2*, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

5 Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one
10 has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker *et al.*, *EMBO J.*, 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an
15 immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for
20 example, Suresh *et al.*, *Methods in Enzymology*, 121:210 (1986).

5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and
25 for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

30 G. Uses for anti-*patched-2* Antibodies

The anti-*patched-2* antibodies of the invention have various utilities. For example, anti-*patched-2* antibodies may be used in diagnostic assays for *patched-2*, *e.g.*, detecting its expression in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either
35 heterogeneous or homogeneous phases [Zola, *Monoclonal Antibodies: A Manual of Techniques*, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a

fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., Nature, 144: 945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Anti-*patched-2* antibodies also are useful for the affinity purification of *patched-2* from recombinant cell culture or natural sources. In this process, the antibodies against *patched-2* are immobilized on a suitable support, such a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the *patched-2* to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the *patched-2*, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the *patched-2* from the antibody.

Basal cell carcinoma (BCC) is the most common human cancer. The *Hh* signaling pathway was found to be activated in all BCCs. Loss of *patched* function is thought to lead to unregulated *Smo* activity and is responsible for about half of all BCCs. *Patched* being a target of the *Hh* pathway itself, increases in *patched* mRNA levels have been detected in BCC [Gailani, et al., Nature Genet. 14: 78-81 (1996)] as well as in animal models of BCC. Oro et al., Science 276: 817-821 (1997); Xie et al., Nature 391: 90-92 (1998). Abnormal activation of *Sh* signaling, such as that which occurs in BCC, was examined to confirm whether *patched-2* expression was increased. As shown in Fig. 9, an *in situ* hybridization for *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) in *Smo*-M2 (SEQ ID NO:16) transgenic mice (Xie et al., *supra*), while lower than *Ptch*, was still high in tumor cells. This suggests that therapeutic antibodies directed toward *Ptch-2* (SEQ ID NO:2) may be useful for the treatment of BCC.

Anti-*patched-2* antibodies also have utilities similar to those articulated for under the previous section "E. Uses of Patched-2". Depending on whether anti-*patched-2* antibodies will bind *patched-2* receptors so as to either inhibit *Hh* signaling (antagonist) or inhibit *patched-2* complexing with *Smo* (SEQ ID NO:17) and thereby remove the normal inhibitory effect of *Smo* (SEQ ID NO:17) on *Hh* signaling (agonist) the antibody will have utilities corresponding to those articulated previously for *patched-2*.

H. Patched-2 Antagonists

Several approaches may be suitably employed to create the *patched-2* antagonist and agonist compounds of the present invention. Any approach where the antagonist molecule can be targeted to the interior of the cell, which interferes or prevents wild type *patched-2* from normal operation is suitable. For example, competitive inhibitors, including mutant *patched-2* receptors which prevent wild type *patched-2* from properly binding with other proteins necessary for *Dhh* and *Hh* signaling. Additional properties of such antagonist or agonist molecules are readily determinable by one of ordinary skill, such as size, charge and hydrophobicity suitable for transmembrane transport.

Where mimics or other mammalian homologues of *patched-2* are to be identified or evaluated, the cells are exposed to the test compound and compared to positive controls which are exposed only to human *patched-2*, and to negative controls which were not exposed to either the compound or the natural ligand. Where antagonists or agonists of *patched-2* signal modulation are to be identified or evaluated, the cells are

exposed to the compound of the invention in the presence of the natural ligand and compared to controls which are not exposed to the test compound.

Detection assays may be employed as a primary screen to evaluate the *Hh* signaling inhibition/enhancing activity of the antagonist/agonist compounds of the invention. The assays may also be used to assess the relative potency of a compound by testing a range of concentrations, in a range from 100 mM to 1 pM, for example, and computing the concentration at which the amount of phosphorylation or signal transduction is reduced or increased by 50% (IC₅₀) compared to controls.

Assays can be performed to identify compounds that affect *Hh* signaling of *patched-2* substrates. Specifically, assays can be performed to identify compounds that increase the phosphorylation activity of *patched-2* or assays can be performed to identify compounds that decrease the *Hh* signaling of *patched-2* substrates. These assays can be performed either on whole cells themselves or on cell extracts. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, cell based assays, etc. Such assay formats are well known in the art.

The screening assays of the present invention are amenable to high-throughput screening of chemical libraries, and are particularly suitable for identifying small molecule drug candidates.

(1) Antagonist and agonist molecules

To screen for antagonists and/or agonists of *patched-2* signaling, the assay mixture is incubated under conditions whereby, but for the presence of the candidate pharmacological agent, *patched-2* induces hedgehog signaling with a reference activity. The mixture components can be added in any order that provides for the requisite hedgehog activity. Incubation may be performed at any temperature that facilitates optimal binding, typically between about 4° and 40°C, more commonly between about 15° and 40°C. Incubation periods are likewise selected for optimal binding but also minimized to facilitate rapid, high-throughput screening, and are typically between about 0.1 and 10 hours, preferably less than 5 hours, more preferably less than 2 hours. After incubation, the effect of the candidate pharmacological agent on the *patched-2* signaling is determined in any convenient way. For cell-free binding-type assays, a separation step is often used to separate bound and unbound components. Separation may, for example, be effected by precipitation (e.g. TCA precipitation, immunoprecipitation, etc.), immobilization (e.g. on a solid substrate), followed by washing. The bound protein is conveniently detected by taking advantage of a detectable label attached to it, e.g. by measuring radioactive emission, optical or electron density, or by indirect detection using, e.g. antibody conjugates.

For example, a method of screening for suitable *patched-2* antagonists and/or agonists could involve the application of *Dhh* and other hedgehog ligands. Such a screening assay could compare *in situ* hybridization in the presence and absence of the candidate antagonist and/or agonist in a *patched-2* expressing tissue as well as confirmation or absence of *patched-2* modulated cellular development.

Typically these methods involve exposing an immobilized *patched-2* to a molecule suspected of binding thereto and determining the level of ligand binding downstream activation of reporter constructs and/or evaluating whether or not the molecule activates (or blocks activation of) *patched-2*. In order to identify such *patched-2* binding ligands, *patched-2* can be expressed on the surface of a cell and used to screen

libraries of synthetic candidate compounds or naturally-occurring compounds (e.g., from endogenous sources such as serum or cells).

Suitable molecules that affect the protein-protein interaction of *patched-2* and its binding proteins include fragments of the latter or small molecules, e.g., peptidomimetics, which will inhibit ligand-receptor interaction. Such small molecules, which are usually less than 10 K molecular weight, are preferable as therapeutics since they are more likely to be permeable to cells, are less susceptible to degradation by various cellular mechanisms, and are not as apt to elicit an immune response as proteins. Small molecules include but are not limited to synthetic organic or inorganic compounds. Many pharmaceutical companies have extensive libraries of such molecules, which can be conveniently screened by using the assays of the present invention. Non-limiting examples include proteins, peptides, glycoproteins, glycopeptides, glycolipids, polysaccharides, oligosaccharides, nucleic acids, bioorganic molecules, peptidomimetics, pharmacological agents and their metabolites, transcriptional and translation control sequences, and the like.

A preferred technique for identifying molecules which bind to *patched-2* utilizes a chimeric substrate (e.g., epitope-tagged *patched-2* or *patched-2* immunoadhesin) attached to a solid phase, such as the well of an assay plate. The binding of the candidate molecules, which are optionally labeled (e.g., radiolabeled), to the immobilized receptor can be measured. Alternatively, competition for various *Hh* pathways, especially *Dhh* (SEQ ID NO:13) can be measured. In screening for antagonists and/or agonists, *patched-2* can be exposed to a *patched-2* substrate followed by the putative antagonist and/or agonist, or the *patched-2* binding protein and antagonist and/or agonist can be added simultaneously, and the ability of the antagonist and/or agonist to block *patched-2* activation can be evaluated.

(2) Detection assays

The *patched-2* polypeptides are useful in assays for identifying lead compounds for therapeutically active agents that modulate *patched-2* receptor/ligand hedgehog signaling. Specifically, lead compounds that either prevent the formation of *patched-2* signaling complexes or prevent or attenuate *patched-2* modulated hedgehog signaling (e.g., binding to *patched-2*) can be conveniently identified.

Various procedures known in the art may be used for identifying, evaluating or assaying the inhibition of activity of the *patched-2* proteins of the invention. As *patched-2* is believed to be a receptor for *Dhh* (SEQ ID NO:13), but also binds *Shh* (SEQ ID NO:14) and *Ihh* (SEQ ID NO:29), techniques known for use with identifying ligand/receptor modulators may also be employed with the present invention. In general, such assays involve exposing target cells in culture to the compounds and a) biochemically analyzing cell lysates to assess the level and/or identity of binding; or (b) scoring phenotypic or functional changes in treated cells as compared to control cells that were not exposed to the test substance. Such screening assays are described in U.S.P. 5,602,171, U.S.P. 5,710,173, WO 96/35124 and WO 96/40276.

(a) Biochemical detection techniques

Biochemical analysis can be evaluated by a variety of techniques. One typical assay mixture which can be used with the present invention contains *patched-2* and a ligand protein with which *patched-2* is normally associated (e.g., *Dhh* (SEQ ID NO:13)) usually in an isolated, partially pure or pure form. One or both of these components may be *patched-2* to another peptide or polypeptide, which may, for example, provide or enhance protein-protein binding, improve stability under assay conditions, etc.

In addition, one of the components usually comprises or is coupled to a detectable label. The label may provide for direct detection by measuring radioactivity, luminescence, optical or electron density, etc., or indirect detection such as an epitope tag, an enzyme, etc. The assay mixture can additionally comprise a candidate pharmacological agent, and optionally a variety of other components, such as salts, buffers, carrier proteins, e.g. albumin, detergents, protease inhibitors, nuclease inhibitors, antimicrobial agents, etc., which facilitate binding, increase stability, reduce non-specific or background interactions, or otherwise improve the efficiency or sensitivity of the assay.

The following detection methods may also be used in a cell-free system wherein cell lysate containing the signal transducing substrate molecule and *patched-2* is mixed with a compound of the invention. To assess the activity of the compound, the reaction mixture may be analyzed by the SDS-PAGE technique or it may be added to substrate-specific anchoring antibody bound to a solid support, and a detection procedure as described above is performed on the separated or captured substrate to assess the presence or absence of a *patched-2* binding ligand. The results are compared to those obtained with reaction mixtures to which the compound is not added. The cell-free system does not require the natural ligand or knowledge of its identity. For example, Posner *et al.* (U.S.P. 5,155,031 describes the use of insulin receptor as a substrate and rat adipocytes as target cells to demonstrate the ability of pervanadate to inhibit PTP activity. Another example, Burke *et al.*, *Biochem. Biophys. Res. Comm.* 204: 129-134 (1994) describes the use of autophosphorylated insulin receptor and recombinant PTP1B in assessing the inhibitory activity of a phosphotyrosyl mimetic.

(i) Whole cell detection

A common technique involves incubating cells with *patched-2* and radiolabeled ligand, lysing the cells, separating cellular protein components of the lysate using an SDS-polyacrylamide gel (SDS-PAGE) technique, in either one or two dimensions, and detecting the presence of labeled proteins by exposing X-ray film. Detection can also be effected without using radioactive labeling. In such a technique, the protein components (e.g., separated by SDS-PAGE) are transferred to a nitrocellulose membrane where the presence of patched-ligand complexes is detected using an anti-ligand antibody.

Alternatively, the anti-*patched-2* ligand antibody can be conjugated with an enzyme, such as horseradish peroxidase, and detected by subsequent addition of a colorimetric substrate for the enzyme. A further alternative involves detecting the anti-*patched-2* ligand by reacting with a second antibody that recognizes anti-*patched-2* ligand, this second antibody being labeled with either a radioactive moiety or an enzyme as previously described. Examples of these and similar techniques are described in Hansen *et al.*, *Electrophoresis* 14: 112-126 (1993); Campbell *et al.*, *J. Biol. Chem.* 268: 7427-7434 (1993); Donato *et al.*, *Cell Growth Diff.* 3: 258-268 (1992); Katagiri *et al.*, *J. Immunol.* 150: 585-593 (1993). Additionally, the anti-*patched-2* ligand can be detected by labeling it with a radioactive substance, followed by scanning the labeled nitrocellulose to detect radioactivity or exposure of X-ray film.

Further detection methods may be developed which are preferred to those described above. Especially for use in connection with high-throughput screening, it is expected that such methods would

exhibit good sensitivity and specificity, extended linear range, low background signal, minimal fluctuation, compatibility with other reagents, and compatibility with automated handling systems.

The *in vivo* efficacy of the treatment of the present invention can be studied against chemically induced tumors in various rodent models. Tumor cell lines propagated in *in vitro* cell cultures can be introduced in experimental rodents, e.g. mice by injection, for example by the subcutaneous route. Techniques for chemical inducement of tumors in experimental animals are well known in the art.

(ii) Kinase assays

Because *patched-2* is a negative regulator of *Hh* signaling, which when activated by *Hh* releases the normal inhibitory effect on *Smo*, the inhibition of *patched-2* binding to *Smo* can be measured by activation of various kinase substrate associated with *Hh* signaling. When the screening methods of the present invention for *patched-2* antagonists/agonists are carried out as an *ex vivo* assay, the target kinase (e.g. *fused*) can be a substantially purified polypeptide. The kinase substrate (e.g., MBP, *Gli*) is a substantially purified substrate, which in the assay is phosphorylated in a reaction with a substantially purified phosphate source that is catalyzed by the kinase. The extent of phosphorylation is determined by measuring the amount of substrate phosphorylated in the reaction. A variety of possible substrates may be used, including the kinase itself in which instance the phosphorylation reaction measured in the assay is autophosphorylation. Exogenous substrates may also be used, including standard protein substrates such as myelin basic protein (MBP); yeast protein substrates; synthetic peptide substrates, and polymer substrates. Of these, MBP and other standard protein substrates may be regarded as preferred. Other substrates may be identified, however, which are superior by way of affinity for the kinase, minimal perturbation of reaction kinetics, possession of single or homogenous reaction sites, ease of handling and post-reaction recover, potential for strong signal generation, and resistance or inertness to test compounds.

Measurement of the amount of substrate phosphorylated in the *ex vivo* assay of the invention may be carried out by means of immunoassay, radioassay or other well-known methods. In an immunoassay measurement, an antibody (such as a goat or mouse anti-phosphoserine/threonine antibody) may be used which is specific for phosphorylated moieties formed during the reaction. Using well-known ELISA techniques, the phosphoserine/threonine antibody complex would itself be detected by a further antibody linked to a label capable of developing a measurable signal (as for example a fluorescent or radioactive label). Additionally, ELISA-type assays in microtitre plates may be used to test purified substrates. Peraldi *et al.*, *J. Biochem.* 285: 71-78 (1992); Schraag *et al.*, *Anal. Biochem.* 211: 233-239 (1993); Cleavland, *Anal. Biochem.* 190: 249-253 (1990); Farley, *Anal. Biochem.* 203: 151-157 (1992) and Lozaro, *Anal. Biochem.* 192: 257-261 (1991).

For example, detection schemes can measure substrate depletion during the kinase reaction. Initially, the phosphate source may be radiolabeled with an isotope such as ^{32}P or ^{33}P , and the amount of substrate phosphorylation may be measured by determining the amount of radiolabel incorporated into the substrate during the reaction. Detection may be accomplished by: (a) commercially available scintillant-containing plates and beads using a beta-counter, after adsorption to a filter or a microtitre well surface, or (b) photometric means after binding to a scintillation proximity assay bead or scintillant plate. Weernink and

Kijken. *J. Biochem. Biophys. Methods* 31: 49, 1996; Braunwalder *et al.*, *Anal. Biochem.* 234: 23 (1996); Kentrup *et al.*, *J. Biol. Chem.* 271: 3488 (1996) and Rusken *et al.*, *Meth. Enzymol.* 200: 98 (1991).

Preferably, the substrate is attached to a solid support surface by means of non-specific or, preferably, specific binding. Such attachment permits separation of the phosphorylated substrate from unincorporated, labeled phosphate source (such as adenosine triphosphate prior to signal detection. In one embodiment, the substrate may be physically immobilized prior to reaction, as through the use of NuncTM high protein binding plate (Hanke *et al.*, *J. Biol. Chem.* 271: 695 (1996)) or Wallac ScintiStripTM plates (Braunwalder *et al.*, *Anal. Biochem.* 234: 23 (1996). Substrate may also be immobilized after reaction by capture on, for example, P81 phosphocellulose (for basic peptides), PEI/acidic molybdate resin or DEAE, or TCA precipitation onto WhatmanTM 3MM paper, Tiganis *et al.*, *Arch. Biochem. Biophys.* 325: 289 (1996); Morawetz *et al.*, *Mol. Gen. Genet.* 250: 17 (1996); Budde *et al.*, *Int J. Pharmacognosy* 33: 27 (1995) and Casnellie, *Meth. Enz.* 200: 115 (1991). Yet another possibility is the attachment of the substrate to the support surface, as by conjugation with binding partners such as glutathione and streptavidin (in the case of GST and biotin), respectively) which have been attached to the support, or via antibodies specific for the tags which are likewise attached to the support.

Further detection methods may be developed which are preferred to those described above. Especially for use in connection with high-throughput screening, it is expected that such methods would exhibit good sensitivity and specificity, extended linear range, low background signal, minimal fluctuation, compatibility with other reagents, and compatibility with automated handling systems.

The *in vivo* efficacy of the treatment of the present invention can be studied against chemically induced tumors in various rodent models. Tumor cell lines propagated in *in vitro* cell cultures can be introduced in experimental rodents, e.g. mice by injection, for example by the subcutaneous route. Techniques for chemical inducement of tumors in experimental animals are well known in the art.

(b) *Biological detection techniques:*

The ability of the antagonist/agonist compounds of the invention to modulate the activity of *patched-2*, which itself modulates *hedgehog* signaling, may also be measured by scoring for morphological or functional changes associated with ligand binding. Any qualitative or quantitative technique known in the art may be applied for observing and measuring cellular processes which comes under the control of *patched-2*. The activity of the compounds of the invention can also be assessed in animals using experimental models of disorders caused by or related to dysfunctional *hedgehog* signaling. For example, ineffective *Dhh* *hedgehog* signaling in mice leads to viable but sterile mice. Additionally, proper *Shh* signaling is critical to murine embryonic development at the notochord and floor plate, neural tube, distal limb structures, spinal column and ribs. Improper *Shh* signaling, is also correlative with cyclopia. Any of these phenotypic properties could be evaluated and quantified in a screening assay for *patched-2* antagonists and/or agonist. Disease states associated with overexpression of *hedgehog* is associated with basal cell carcinoma while inactive *Shh* signaling leads to improper neural development.

The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosages for use in humans. The dosage of the compounds of the invention should lie within a range

of circulating concentrations with little or no toxicity. The dosage may vary within this range depending on the dosage form employed and the route of administration.

(2) *Antisense oligonucleotides*

Another preferred class of antagonists involves the use of gene therapy techniques, include the administration of antisense oligonucleotides. Applicable gene therapy techniques include single or multiple administrations of therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. Reference short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by restricted uptake by the cell membrane, Zamecnik *et al.*, *Proc. Natl. Acad. Sci. USA* 83: 4143-4146 (1986). The anti-sense oligonucleotides can be modified to enhance their uptake, e.g., by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques known for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, *ex vivo*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection, Dzurik *et al.*, *Trends Biotech.* 11: 205-210 (1993). In some situations it is desirable to provide the nucleic acid source with an agent that targets the cells, such as an antibody specific for a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g., capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, and proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu *et al.*, *J. Biol. Chem.* 262: 4429-4432 (1987); Wagner *et al.*, *Proc. Natl. Acad. Sci. USA* 87: 3410-3414 (1990). For a review of known gene targeting and gene therapy protocols, see Anderson *et al.*, *Science* 256: 808-813 (1992).

In one embodiment of the invention, *patched-2* expression may be reduced by providing *patched-2*-expressing cells with an amount of *patched-2* antisense RNA or DNA effective to reduce expression of the *patched-2* protein.

I. Diagnostic Uses

Another use of the compounds of the invention (e.g., *patched-2*, *patched-2* and anti-*patched-2* antibodies) described herein is to help diagnose whether a disorder is driven, to some extent, by *patched-2* or hedgehog signaling. For example, basal cell carcinoma cells are associated with active hedgehog signaling, spermatocyte formation is associated with *Dhh* signaling, and defective *patched* and *patched-2* suppression may be associated with testicular carcinomas.

A diagnostic assay to determine whether a particular disorder is driven by *patched-2* modulated hedgehog signaling, can be carried out using the following steps: (1) culturing test cells or tissues; (2) administering a compound which can prevent *patched-2* binding with *Smo* (SEQ ID NO:17), thereby activating the *Hh* signaling pathway; and (3) measuring the amount of *Hh* signaling. The steps can be carried

out using standard techniques in light of the present disclosure. For example, standard techniques can be used to isolate cells or tissues and culturing or *in vivo*.

Compounds of varying degree of selectivity are useful for diagnosing the role of *patched-2*. For example, compounds which inhibit *patched-2* in addition to another form of kinase can be used as an initial test compound to determine if one of several signaling ligands drive the disorder. The selective compounds can then be used to further eliminate the possible role of the other ligands in driving the disorder. Test compounds should be more potent in inhibiting ligand-*patched-2* binding activity than in exerting a cytotoxic effect (e.g., an IC_{50}/LD_{50} of greater than one). The IC_{50} and LD_{50} can be measured by standard techniques, such as an MTT assay, or by measuring the amount of LDH released. The degree of IC_{50}/LD_{50} of a compound should be taken into account in evaluating the diagnostic assay. For example, the larger the IC_{50}/LD_{50} ratio the more relative the information. Appropriate controls take into account the possible cytotoxic effect of a compound of a compound, such as treating cells not associated with a cell proliferative disorder (e.g., control cells) with a test compound, can also be used as part of the diagnostic assay. The diagnostic methods of the invention involve the screening for agents that modulate the effects of *patched-2* upon *hedgehog* signaling. Exemplary detection techniques include radioactive labeling and immunoprecipitating (U.S.P. 5,385,915).

J. Pharmaceutical Compositions and Dosages

Therapeutic formulations of the compositions of the invention are prepared for storage as lyophilized formulations or aqueous solutions by mixing the *patched-2* molecule, agonist and/or antagonist having the desired degree of purity with optional "pharmaceutically-acceptable" or "physiologically-acceptable" carriers, excipients or stabilizers typically employed in the art (all of which are termed "excipients"). For example, buffering agents, stabilizing agents, preservatives, isotonicifiers, non-ionic detergents, antioxidants and other miscellaneous additives. (See Remington's Pharmaceutical Sciences, 16th Ed., A. Osol, Ed. (1980)). Such additives must be nontoxic to the recipients at the dosages and concentrations employed.

Buffering agents help to maintain the pH in the range which approximates physiological conditions. They are preferably present at concentration ranging from about 2mM to about 50 mM. Suitable buffering agents for use with the present invention include both organic and inorganic acids and salts thereof such as citrate buffers (e.g., monosodium citrate-disodium citrate mixture, citric acid-trisodium citrate mixture, citric acid-monosodium citrate mixture, etc.), succinate buffers (e.g., succinic acid-monosodium succinate mixture, succinic acid-sodium hydroxide mixture, succinic acid-disodium succinate mixture, etc.), tartrate buffers (e.g., tartaric acid-sodium tartrate mixture, tartaric acid-potassium tartrate mixture, tartaric acid-sodium hydroxide mixture, etc.), fumarate buffers (e.g., fumaric acid-monosodium fumarate mixture, etc.), fumarate buffers (e.g., fumaric acid-monosodium fumarate mixture, fumaric acid-disodium fumarate mixture, monosodium fumarate-disodium fumarate mixture, etc.), gluconate buffers (e.g., gluconic acid-sodium glyconate mixture, gluconic acid-sodium hydroxide mixture, gluconic acid-potassium glyconate mixture, etc.), oxalate buffer (e.g., oxalic acid-sodium oxalate mixture, oxalic acid-sodium hydroxide mixture, oxalic acid-potassium oxalate mixture, etc.), lactate buffers (e.g., lactic acid-sodium lactate mixture, lactic acid-

sodium hydroxide mixture, lactic acid-potassium lactate mixture, etc.) and acetate buffers (e.g., acetic acid-sodium acetate mixture, acetic acid-sodium hydroxide mixture, etc.). Additionally, there may be mentioned phosphate buffers, histidine buffers and trimethylamine salts such as Tris.

Preservatives are added to retard microbial growth, and are added in amounts ranging from 0.2% - 1% (w/v). Suitable preservatives for use with the present invention include phenol, benzyl alcohol, *meta*-cresol, methyl paraben, propyl paraben, octadecyldimethylbenzyl ammonium chloride, benzalconium halides (e.g., chloride, bromide, iodide), hexamethonium chloride, alkyl parabens such as methyl or propyl paraben, catechol, resorcinol, cyclohexanol, and 3-pentanol.

Isotonifiers sometimes known as "stabilizers" are present to ensure isotonicity of liquid compositions of the present invention and include polyhydric sugar alcohols, preferably trihydric or higher sugar alcohols, such as glycerin, erythritol, arabitol, xylitol, sorbitol and mannitol. Polyhydric alcohols can be present in an amount between 0.1% to 25% by weight, preferably 1% to 5% taking into account the relative amounts of the other ingredients.

Stabilizers refer to a broad category of excipients which can range in function from a bulking agent to an additive which solubilizes the therapeutic agent or helps to prevent denaturation or adherence to the container wall. Typical stabilizers can be polyhydric sugar alcohols (enumerated above); amino acids such as arginine, lysine, glycine, glutamine, asparagine, histidine, alanine, ornithine, L-leucine, 2-phenylalanine, glutamic acid, threonine, etc., organic sugars or sugar alcohols, such as lactose, trehalose, stachyose, mannitol, sorbitol, xylitol, ribitol, myoinositol, galactitol, glycerol and the like, including cyclitols such as inositol; polyethylene glycol; amino acid polymers; sulfur containing reducing agents, such as urea, glutathione, thiocitic acid, sodium thioglycolate, thioglycerol, α -monothioglycerol and sodium thio sulfate; low molecular weight polypeptides (i.e. < 10 residues); proteins such as human serum albumin, bovine serum albumin, gelatin or immunoglobulins; hydrophilic polymers, such as polyvinylpyrrolidone monosaccharides, such as xylose, mannose, fructose, glucose; disaccharides such as lactose, maltose, sucrose and trisaccharides such as raffinose; polysaccharides such as dextran. Stabilizers can be present in the range from 0.1 to 10,000 weights per part of weight active protein.

Non-ionic surfactants or detergents (also known as "wetting agents") are present to help solubilize the therapeutic agent as well as to protect the therapeutic protein against agitation-induced aggregation, which also permits the formulation to be exposed to shear surface stressed without causing denaturation of the protein. Suitable non-ionic surfactants include polysorbates (20, 80, etc.), polyoxamers (184, 188 etc.), Pluronic® polyols, polyoxyethylene sorbitan monoethers (Tween®-20, Tween®-80, etc.). Non-ionic surfactants are present in a range of about 0.05 mg/ml to about 1.0 mg/ml, preferably about 0.07 mg/ml to about 0.2 mg/ml.

Additional miscellaneous excipients include bulking agents, (e.g. starch), chelating agents (e.g. EDTA), antioxidants (e.g., ascorbic acid, methionine, vitamin E), and cosolvents.

The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely

affect each other. For example, it may be desirable to further provide an immunosuppressive agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsule prepared, for example, by coascervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsule and poly-(methylmethacrylate) microcapsule, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in *Remington's Pharmaceutical Sciences*, 16th edition, A. Osal, Ed. (1980).

The formulations to be used for in vivo administration must be sterile. This is readily accomplished, for example, by filtration through sterile filtration membranes.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi-permeable matrices of solid hydrophobic polymers containing the compounds of the invention, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No.3,773,919), copolymers of L-glutamic acid and ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated compounds of the invention remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

The amount of therapeutic polypeptide, antibody or fragment thereof which will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. Where possible, it is desirable to determine the dose-response curve and the pharmaceutical compositions of the invention first *in vitro*, and then in useful animal model systems prior to testing in humans. However, based on common knowledge of the art, a pharmaceutical composition effective in modulating *Dhh* and *Hh* signaling may provide a local *patched-2* protein concentration of between about 10 and 1000 ng/ml, preferably between 100 and 800 ng/ml and most preferably between about 200 ng/ml and 600 ng/ml of *Ptch-2* (SEQ ID NO:2).

In a preferred embodiment, an aqueous solution of therapeutic polypeptide, antibody or fragment thereof is administered by subcutaneous injection. Each dose may range from about 0.5 µg to about 50 µg per kilogram of body weight, or more preferably, from about 3 µg to about 30 µg per kilogram body weight.

The dosing schedule for subcutaneous administration may vary from once a week to daily depending on a number of clinical factors, including the type of disease, severity of disease, and the subject's sensitivity to the therapeutic agent.

Patched-2 polypeptide may comprise an amino acid sequence or subsequence thereof as indicated in Fig. 1, active amino acid sequence derived therefrom, or functionally equivalent sequence as this subsequence is believed to comprise the functional portion of the *patched-2* polypeptide.

If the subject manifests undesired side effects such as temperature elevation, cold or flu-like symptoms, fatigue, etc., it may be desirable to administer a lower dose at more frequent intervals. One or more additional drugs may be administered in combination with *patched-2* to alleviate such undesired side effects, for example, an anti-pyretic, anti-inflammatory or analgesic agent.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Rockville, Maryland.

EXAMPLE I

Introduction

At the cell surface, *Hh* function appears to be mediated by a multicomponent receptor complex involving *Ptch* and *Smo* (SEQ ID NO:17), two multi-transmembrane proteins initially identified as segment polarity genes in *Drosophila* and later characterized in vertebrates. Nakano, Y. *et al.*, *Nature* **341**: 508-513 (1989); Goodrich *et al.*, *Gene Dev.* **10**: 301-312 (1996); Marigo *et al.*, *Develop.* **122**: 1225-1233 (1996); van den Heuvel *et al.*, *Nature* **382**: 547-551 (1996); Alcedo *et al.*, *Cell* **86**: 221-232 (1996); Stone *et al.*, *Nature* **384**: 129-134 (1996). Both genetic and biochemical evidence support the existence of a receptor complex where *Ptch* (SEQ ID NO:4) is the ligand binding subunit, and where *Smo* (SEQ ID NO:17), a G-protein coupled receptor-like molecule, is the signaling component. Stone *et al.*, *Nature* **384**: 129-134 (1996), Marigo *et al.*, *Nature* **384**: 176-79 (1996), Chen *et al.*, *Cell* **87**: 553-63 (1996). Upon binding of *Hh* to *Ptch* (SEQ ID NO:4), the normal inhibitory effect of *Ptch* (SEQ ID NO:4) on *Smo* (SEQ ID NO:17) is relieved, allowing *Smo* (SEQ ID NO:17) to transduce the *Hh* signal across the plasma membrane.

Results

It remains to be established if the *PTCH/SMO* receptor complex mediates the action of all 3 mammalian *Hhs* or if specific components exist. Recently, a second murine *Patched* gene, *mPatched-2* (SEQ ID NO:7) was recently isolated [Motoyama *et al.*, *Nature Genet.* **18**: 104-106 (1998)] but its function as a *Hh* receptor has not been established. In order to characterize *patched-2* (SEQ ID NO:2) and compare it to *Patched* (SEQ ID NO:4) with respect to the biological function of the various *Hh* family members, we have screened EST databases with the *Patched* (SEQ ID NO:4) protein and identified 2 EST candidates for a

novel human *patched* gene. A full length cDNA encoding human *Ptch-2* (SEQ ID NO:2) was cloned from a testis library. The initiation ATG defines a 3612 nucleotide open reading frame encoding a 1204 amino acid long protein with a predicted molecular weight of approximately 131 kDa. The overall identity between human *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) is 54% (Fig. 1), while the identity between human *PTCH-2* and the recently described mouse *Ptch-2* (SEQ ID NO:7) is 90% (Fig. 8). The most obvious structural difference between the two human *Patched* proteins is a truncated C-terminal cytoplasmic domain in *Ptch-2* (SEQ ID NO:2). In addition, only one of the two glycosylation sites present in *Ptch* (SEQ ID NO:4) is conserved in *Ptch-2* (SEQ ID NO:2).

To determine if *Patched-2* is a *Hh* receptor and if the two *Patched* molecules are capable of discriminating between the various *Hh* ligands through specific binding, Applicants transfected human 293 embryonic kidney cells with *Ptch* (SEQ ID NO:4) or *Ptch-2* (SEQ ID NO:2) expression constructs and analyzed the cells for binding of *Shh*, *Dhh* and *Ihh*. As shown on Figure 7A, binding of ^{125}I -*Shh* can be competed with an excess of *Shh*, *Dhh* or *Ihh* (SEQ ID NOS: 14, 13 and 29), respectively. Scatchard analysis of the displacement curves indicates that all *Hhs* have similar affinity for *Ptch* (SEQ ID NO:4) (*Shh*, 1.0nM (SEQ ID NO:14); *Dhh*, 2.6nM (SEQ ID NO:13); *Ihh*, 1.0nM (SEQ ID NO:29) and *Ptch-2* (SEQ ID NO:2) (*Shh*, 1.8nM (SEQ ID NO:14); *Dhh*, 0.6nM (SEQ ID NO:13); *Ihh*, 0.4nM (SEQ ID NO:29) indicating that both *PTCH* (SEQ ID NO:4) and *PTCH-2* (SEQ ID NO:2) can serve as physiological receptors for the 3 mammalian *Hh* proteins.

Applicants next determined whether, like *Patched*, *Patched-2* forms a physical complex with *Smo* (SEQ ID NO:17). Expression constructs for Flag-tagged *Ptch* (SEQ ID NO:4) or *Ptch-2* (SEQ ID NO:2) were transiently co-transfected in 293 cells with Myc-tagged *Smo* (SEQ ID NO:17). As described previously [Stone *et al.*, *Nature* 384: 129-34 (1996)], in cells expressing *Ptch* (SEQ ID NO:4) and *Smo* (SEQ ID NO:15), *Ptch* (SEQ ID NO:4) can be immunoprecipitated with antibodies against the epitope-tagged *Smo* (SEQ ID NO:15) (Fig. 7B). Similarly, *Patched-2* can be immunoprecipitated with antibodies against the epitope-tagged *Smo* (SEQ ID NO:15) when the two proteins are co-expressed in 293 cells. Together, these results suggest a model where *Patched-2* forms a multicomponent *Hh* receptor complex with *Smo* (SEQ ID NO:17) similar to the one described for *PTCH* (Stone *et al.*, *supra*). Interestingly, these results also demonstrate that the long C-terminal tail which is missing in *Patched-2* is not required for the interaction with *Smo* (SEQ ID NO:17) as was already suggested by the analysis of truncated *Patched* (Stone *et al.*, *supra*). However, it remains possible that the absence of a C-terminal domain affects the capacity of *Patched-2* to block signaling by *Smo* (SEQ ID NO:17) or leads to difference in signaling by *Patched* compared to *Patched-2*.

To further investigate whether *Patched-2* could mediate the action of a specific *Hh* molecule based on its expression profile, Applicants have compared the expression pattern of *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2). First, Northern blot analysis using a probe specific for *Ptch-2* (SEQ ID NO:1) revealed high levels of *PTCH2* mRNA in the testis (Fig. 4). By this method, *Ptch-2* (SEQ ID NO:1) expression was not detected in any other tissue analyzed including embryonic tissues (data not shown). This profile is very different from the one observed for *Ptch* (SEQ ID NO:18) which was not found in testis by Northern blot but in a large number of adult and embryonic tissues [Goodrich *et al.*, *Genes Dev.* 10: 301-312

(1996)]. More detailed analysis of the expression pattern of *Ptch* (SEQ ID NO:18) and *Ptch-2* (SEQ ID NO:1) was performed by *in situ* hybridization with particular attention to testis. As previously described (Motoyama *et al.*, *supra*), low levels of *Ptch-2* (SEQ ID NO:1) expression were detected in epithelial cells of the developing tooth and skin (data not shown). High levels of *Ptch-2* (SEQ ID NO:2) encoding mRNA are expressed inside the seminiferous tubule, on the primary and secondary spermatocytes (Fig. 6B,6E) while only low levels of *Ptch* (SEQ ID NO:4) encoding mRNA can be detected on the Leydig cells located in the interstitium of the seminiferous tubules (Fig. 6A). The primary and secondary spermatocytes are in close contact with the supporting Sertoli cells, the source of *Dhh* (SEQ ID NO:13) in the testis [Bitgood *et al.*, *Curr. Biol.* 6: 298-304 (1996)]. To determine which one of the 2 receptors is the most relevant mediator of *Dhh* (SEQ ID NO:13) activity in the testis, we have analyzed the expression profile of FuRK (SEQ ID NO:10), a Fused Related Kinase that is believed to be a component of the *Hh* signaling pathway. Consistent with the idea that *Patched-2* is the target of *Dhh* in the testis, we found that FuRK (SEQ ID NO:10) is expressed only in germ cells where it colocalizes with *Ptch-2* (SEQ ID NO:2) (Figure 4c,f). *Dhh* (SEQ ID NO:13) is required for proper differentiation of germ cells since male *Dhh*-deficient mice are sterile due to lack of mature sperm (Bitgood *et al.*, *supra*). Our data suggest that *Dhh* (SEQ ID NO:13) acts directly on germ cells through *Ptch-2* (SEQ ID NO:2) while the function of *Ptch* (SEQ ID NO:4) expressed at low levels on testosterone producing Leydig cells is unclear.

Discussion

Loss of heterozygosity (LOH) for *Patched* was reported to occur with high frequency in familial as well as sporadic basal cell carcinoma [Johnson *et al.*, *Science* 272: 1668-71 (1996); Hahn *et al.*, *Cell* 85: 841-51 (1996); Gailani *et al.*, *Nature Genetics* 14: 78-81; Xie *et al.*, *Cancer Res.* 57: 2369-72 (1997)], suggesting that it functions as a tumor suppressor. According to the receptor model described above, loss of *Patched* function may result in aberrant signaling by *Smo* (SEQ ID NO:17), leading to hyperproliferation of the skin basal cell layer. If, as suggested above, *Patched-2* mediates the function of *Dhh*, loss of *Patched-2* may lead to tumor formation in tissues where *Smo* (SEQ ID NO:17) activity is controlled by *Patched-2*. The gene encoding *Ptch-2* (SEQ ID NO:2) was mapped by fluorescence *in situ* hybridization and by PCR using a radiation hybrid panel to human chromosome 1p33-34 (data not shown). Interestingly, recent analysis of recurrent chromosomal abnormalities in testicular tumors, including seminomas, revealed a deletion of the region 1p32-36 [Summersgill *et al.*, *B. J. Cancer* 77: 305-313 (1998)]. Loss of this region encompassing the *Patched-2* locus was consistent in 36% of the germ cell tumor cases. These data raise the possibility that, like *Patched* in basal cell carcinoma and medulloblastoma, *Patched-2* may be a tumor suppressor in *Dhh* (SEQ ID NO: 13) target cells such as spermatocytes, further implicating *Hh* signaling in cancer.

In summary, our data demonstrate that both *Patched* and *Patched-2* are genuine *Hh* receptors and that they are both capable of forming a complex with *Smo* (SEQ ID NO:17). Although binding data indicate that *Patched* and *Patched-2* do not discriminate between the various *Hh* ligands through affinity differences, the distinct tissue distribution of these 2 receptors suggests that *in vivo*, *Patched* may be the primary receptor for *Shh* whereas *Patched-2* will mediate mainly *Dhh* signaling. The function of *Patched* expression in Leydig cells in the absence of some of the *Hh* signaling components remain to be explained. Similarly, it will be of interest to determine if *Patched-2* plays a role when expressed in *Shh* expressing cells present in the

developing tooth and skin Motoyama *et al.*, *Nature Genet.* **18**: 104-106 (1998). Finally, the existence of *Patched-2* raises the question of whether additional *patched* receptors exist, in particular one that mediates the function of *Ihh* (SEQ ID NO: 29).

Material and Methods

1. Isolation of human *patched-2* cDNA clones

An expressed sequence tag (EST) DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA) was searched for a human homologue of the *Drosophila* segment polarity gene *patched-2*. Two ESTs (Incyte #905531 and 1326258) (Fig. 2) were identified as a potential candidates. In order to identify human cDNA libraries containing human *patched-2* clones, human cDNA libraries in pRK5 were first screened by PCR using the following primers:

5'-905531(A): 5'-AGGCGGGGGATCACAGCA-3' (SEQ ID NO:19)

3'-905531(A): 5'-ATACCAAAGAGTTCCACT-3' (SEQ ID NO:20)

A fetal lung library was selected and enriched for *patched-2* cDNA clones by extension of single stranded DNA from plasmid libraries grown in dut⁻/ung⁻ host using the 3'-905531(A) primer in a reaction containing 10µl of 10x PCR Buffer (Klentaq®), 1µl dNTP (200 µM), 1 µl library DNA (200 ng), 0.5 µl primer, 86.5 µl H₂O and 1 µl of Klentaq® (Clontech) added after a hot start. The reaction was denatured for 1 min. at 95°C,

annealed for 1 min. at 60°C then extended for 20 min. at 72°C. DNA was extracted with phenol/CHCl₃, ethanol precipitated, then transformed by electroporation into DH10B (Gibco/BRL) host bacteria. Colonies from each transformation were replica plated on nylon membranes and screened with an overlapping oligo probe derived from the EST sequence (#905531) of the following sequence:

5'-ptch2 probe: 5'-CTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGTGC-3' (SEQ ID NO:21)

3'-ptch2probe: 5'-AGAGCACAGACGAGGAAAGTGCACACCAGCAGGATGCAGACGGCC-3' (SEQ ID NO:22)

The oligo probe was labeled with [γ -³²P]-ATP and T4 polynucleotide kinase. Filters were hybridized overnight at 42°C in 50% formamide, 5xSSC, 10xDenhardt's, 0.05M sodium phosphate (pH 6.5), 0.1% sodium pyrophosphate, 50 µg/ml of sonicated salmon sperm DNA. The filters were then rinsed in 2x SSC and washed in 0.1x SSC, 0.1% SDS then exposed to Kodak® X Ray films. Using this procedure, a partial clone was isolated from the fetal brain library (clone 3A – Fig. 10) (SEQ ID NO:8). In order to isolate the missing 5'-sequence, a testis library (see northern blot analysis, *infra*) was screened. The primer set used to amplify a 204 bp probe from clone 3A to probe the testis library was:

RACE 5: 5'-ACTCCTGACTTGTAGCAGATT-3' (SEQ ID NO. 23) and

RACE 6: 5'-AGGCTGCATACACCTCTCAGA-3' (SEQ ID NO:24).

The amplified probe was purified by excision from an agarose gel and labeled with a random primer labeling kit (Boehringer Mannheim). Several clones were isolated, including one (clone 16.1 – Fig. 11) (SEQ ID NO:9) containing a potential initiation methionine. A full length cDNA encoding a *Patched-2* was reconstructed by assembling several of these clones. The full length cDNA encoding human *Pitch-2* (Fig. 1

(SEQ ID NO:1)) has a 3612 nucleotide long open reading frame encoding a 1204 amino acid protein with a 144 kDa predicted molecular weight. Alignment with human *Ptch* (SEQ ID NO:4) reveals a 53% identity between the 2 molecules at the amino acid level (Fig. 3). All 12 transmembrane domains are conserved. The most significant difference is a shorter C-terminal intracellular domain in *Ptch-2* (SEQ ID NO:2) compared to *Ptch* (SEQ ID NO:4).

2. Northern blot analysis:

In order to determine the best tissue source for isolation of the complete full length *Patched-2* cDNA as well as to determine its expression profile, we probed human multiple tissue northern blots (Clontech) with a 752 bp fragment amplified from the 3' untranslated region of *Patched-2* using the following primers:

TM2: TM2 5-GCTTAGGCCCCGAGGAGAT-3' (SEQ ID NO:25)

UTR2: 5'-AACTCACAACCTTCTCTCCA-3' (SEQ ID NO:26).

The resulting fragment was gel purified and labeled by random priming. The blots were hybridized in ExpressHyb[®] hybridization solution (Clontech) in the presence of 1×10^6 cpm/ml ³²P-labeled probe at 42°C overnight. The blots were washed in 2x SSC at room temperature for 10 minutes and washed in 0.1 x SSC/0.1 % SDS at 42°C for 30 minutes then exposed to x-ray film overnight. Fig. 4 shows that *Ptch-2* message is expressed at high levels in only the testis.

3. Chromosomal localization:

The primers TM2 (SEQ ID NO:25) and UTR2 (SEQ ID NO:26) described above were used to screen the Genome Systems (St. Louis, MO) BAC library. Two individual BAC clones were obtained from this library and chromosomal localization of both of the clones by FISH indicated that *Ptch-2* (SEQ ID NO:2) maps to human chromosome 1p33-34 (FIG 5). Loss of heterozyosity (LOH) for *Patched* was reported to occur with high frequency in basal cell carcinoma. Loss of *Patched* function is thought to lead to constitutive signaling by Smoothed (Smo) (SEQ ID NO:17), resulting in hyperproliferation of the basal layer of the dermis. A similar mechanism may lead to the formation of germ cell tumors. This model proposes that the first step in the progression of a germ cell tumor is an initial loss of DNA by a germ cell precursor, leading to a neoplastic germ cell which then forms a seminoma [De Jong *et al.*, *Cancer Genet. Cytogenet.* **48**: 143-167 (1990)]. From the invasive seminoma, all other forms of germ cell tumor types develop. Approximately 80% of all germ cell tumors correlate with an isochromosome 12p (i12p) and is found at a higher frequency in non-seminomas than seminomas [Rodriguez *et al.*, *Cancer Res.* **52**: 2285-2291 (1992)]. However, analysis of recurrent chromosomal abnormalities in testicular tumors including seminomas revealed a deletion of the region 1p32-36. Loss of this region was consistent in 36% of the germ cell tumor cases of in a recent study Summersgill *et al.*, *B. J. Cancer* **57**: 305-313 (1998)]. A similar deletion of chromosome 1p32-36 has been reported at a frequency of 28% in oligodendrogliomas; Bello, *et al.*, *Int. J. Cancer* **57**: 172-175 (1994). While expression of *Ptch-2* (SEQ ID NO:2) in the brain was not examined here in detail, *Ptch-2* (SEQ ID NO:2) is thought to be the *Dhh* receptor (see below) and expression of *Dhh* by murine Schwann cells was previously reported [Bitgood *et al.*, *Develop. Biol.* **172**: 126-138 (1995)]. Since *Ptch-2* (SEQ ID NO:2) localizes to chromosome 1p33-34 it is possible that *Patched-2*

regulates *Smo* (SEQ ID NO:17) signaling in *Dhh* target cells and that loss of *Patched-2* function leads to abnormal *Smo* (SEQ ID NO:17) signaling in these cells and subsequent tumor formation.

4. *In situ* hybridization:

Mouse testis sections were cut at 16 μ m, and processed for *in situ* hybridization by the method described in Phillips *et al.*, *Science* 250: 290-294 (1990). ³³P-UTP labeled RNA probes were generated as described in Melton *et al.*, *Nucleic Acids Res.* 12: 7035-7052 (1984). Sense and antisense probes were synthesized from the 3' non-coding region of the mouse *Patched* or *Patched-2* and from a mouse FuRK cDNA fragment corresponding to the region encoding amino acid 317-486 of the human sequence using T3 and T7, respectively.

10 PTCH:

503 (Anti-sense)

5'GGATTCTAATACGACTCACTATAGGGCCCAATGGCCTAAACCGACTGC3' (SEQ ID NO:27)

503 (Sense)

5'CTATGAAATTAACCCTCACTAAAGGGACCCACGGCCTCTCCTCACA3' (SEQ ID NO:28)

15 PTCH2:

504 (Anti-sense)

5'GGATTCTAATACGACTCACTATAGGGCCCCTAAACTCCGCTGCTCCAC3' (SEQ ID NO:12)

504 (Sense)

5'CTATGAAATTAACCCTCACTAAAGGGAGCTCCCGTGAGTCCCTATGTG3' (SEQ ID NO:11)

20 FuRK sense and antisense were synthesized from a mouse fused DNA fragment using T3 and T7, respectively, corresponding to the region encoding amino acid residues 317-486 of the human.

Figure 6 illustrates that, although both *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2) are expressed in testis, their expression pattern does not overlap. *Ptch* (SEQ ID NO:4) is expressed in the Leydig cells of the interstitium while *Ptch-2* (SEQ ID NO:2) is expressed in the primary and secondary spermatocytes.

The expression of *Patched-2* specifically in the developing spermatogonia suggest that *Patched-2* is the immediate target of *Dhh* (SEQ ID NO. 13). *Dhh* (SEQ ID NO. 13) is expressed by Sertoli cells and mice deficient in *Dhh* (SEQ ID NO. 13) are sterile because of a defect in sperm production [Bitgood *et al.*, *Curr. Biol.* 6: 298-304 (1996)]. Although this effect on germ cells was thought to be indirect and mediated by *Patched* present on Leydig cells, our data suggest that *Dhh* directly acts on germ cells through *Patched-2*. This is further demonstrated by the localization of FuRK (SEQ ID NO. 10), an intracellular kinase homologous to *Drosophila* Fused and involved in transducing the Hedgehog (*Hh*) signal. As shown in Figure 6, FuRK (SEQ ID NO:10) is colocalizes with *Ptch-2* (SEQ ID NO:2) in germ cells and not with *Ptch* (SEQ ID NO:4) in Leydig cells, suggesting that *Patched-2* and not *Patched* will be able to transduce the *Dhh* signal. These results suggest that *Patched-2* is a *Dhh* receptor.

Ptch-2 mRNA levels in *Smo*-M2 (SEQ ID NO. 16) transgenic mice [a *Smo* mutation which results in autonomous phenotypes similar to BCC, Xie *et al.*, *Nature* 391: 90-92 (1998)] can be increased upon

abnormal activation of the *Hh* signaling pathway. As indicated in Fig. 9, *Ptch-2* (SEQ ID NO:2) levels were high in tumor cells (although lower than *Ptch* (SEQ ID NO:4) levels). This suggests that antibodies directed toward *Ptch-2* (SEQ ID NO:2) may be useful in the treatments of BCC.

5. Immunoprecipitation with *Smo*:

5 The binding of *Patched-2* to *Smo* (SEQ ID NO:17) was assessed by cotransfection using a transient transfection system of a myc-epitope tagged *Smo* (SEQ ID NO:15) and a FLAG-epitope tagged *Patched* or *Patched-2* expression construct in 293 cells using standard techniques (Gorman, C., *DNA Cloning: A Practical Approach*, Clover, DM ed., Vol. 11, pp. 143-190, IRL Press, Washington, D.C.). 36 hours after transfection, the cells were lysed in 1% NP-40 and immunoprecipitated overnight with the 9E10 anti-myc antibody or with the M2 anti-FLAG antibody (IBI-Kodak) followed by protein A Sepharose, and then separated on a denatured 6% polyacrylamide gel. Proteins were detected by transfer to nitrocellulose and probing with antibodies to Flag or Myc epitopes, using the ECL detection system (Amersham). Figure 7B indicates that both *Ptch* (SEQ ID NO:4) or *Ptch-2* (SEQ ID NO:2) are expressed at the same level (IP Flag, Blot Flag) and that like *Ptch* (SEQ ID NO:4), *Ptch-2* (SEQ ID NO:2) forms a physical complex with *Smo* (SEQ ID NO:17). These results suggest that like *Patched*, *Patched-2* controls *Hh* signaling through its interaction with *Smo* (SEQ ID NO:17).

6. *Hh* Binding:

To determine whether *Patched-2* is able to bind to the various hedgehog ligands, 293 cells were transfected with *Ptch* (SEQ ID NO:4) or *Ptch-2* (SEQ ID NO:2) using standard procedures. Cells were incubated with 100 pM ¹²⁵I-*Shh* (19kD amino terminal fragment of murine *Shh* (SEQ ID NO:14)) in the presence or absence of excess unlabeled *Shh* (SEQ ID NO:14) or *Dhh* (SEQ ID NO:13) for 2h at room temperature. After equilibrium was reached, the ligand bound cells were centrifuged through a continuous sucrose gradient to separate unincorporated and then counted in a scintillation counter. Figure 7A shows that both *Dhh* (SEQ ID NO:13) and *Shh* (SEQ ID NO:14) bind to *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2). Varying concentrations of cold competitor indicate that the 2 ligands have similar affinity for *Ptch* (SEQ ID NO:4) and *Ptch-2* (SEQ ID NO:2).

Example 2

Expression of *patched-2* in *E. coli*

The DNA sequence encoding human *patched-2* is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites that correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar *et al.*, *Gene*, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences that encode for an antibiotic resistance gene, a *trp* promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the vertebrate *patched-2* coding region, lambda transcriptional terminator, and an *argU* gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook *et al.*, *supra*. Transformants are identified by their ability to grow on LB plates and antibiotic

resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized vertebrate *patched-2* protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

Example 3

Expression of patched-2 in mammalian cells

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the vertebrate patched-2 DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the vertebrate patched-2 DNA using ligation methods such as described in Sambrook *et al.*, *supra*. The resulting vector is called pRK5-patched-2.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μ g pRK5-patched-2 DNA is mixed with about 1 μ g DNA encoding the VA RNA gene [Thimmappaya *et al.*, *Cell*, 31:543 (1982)] and dissolved in 500 μ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl_2 . To this mixture is added, dropwise, 500 μ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO_4 , and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in FBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 $\mu\text{Ci/ml}$ ^{35}S -cysteine and 200 $\mu\text{Ci/ml}$ ^{35}S -methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of vertebrate *patched-2* polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, vertebrate *patched-2* may be introduced into 293 cells transiently using the dextran sulfate method described by Sompayrac *et al.*, *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μ g pRK5-patched-2 DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 $\mu\text{g/ml}$ bovine insulin and 0.1 $\mu\text{g/ml}$ bovine transferrin. After about four days, the

c nditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed vertebrate *patched-2* can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, vertebrate *patched-2* can be expressed in CHO cells. The pSVi-*patched-2* can be transfected into CHO cells using known reagents such as CaPO_4 or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S -methionine. After determining the presence of vertebrate *patched-2* polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed vertebrate *patched-2* can then be concentrated and purified by any selected method.

Epitope-tagged vertebrate *patched-2* may also be expressed in host CHO cells. The vertebrate *patched-2* may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into an expression vector. The poly-his tagged vertebrate *patched-2* insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged vertebrate *patched-2* can then be concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

Example 4

Expression of vertebrate *patched-2* in Yeast

The following method describes recombinant expression of vertebrate *patched-2* in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of vertebrate *patched-2* from the ADH2/GAPDH promoter. DNA encoding vertebrate *patched-2*, a selected signal peptide and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of vertebrate *patched-2*. For secretion, DNA encoding vertebrate *patched-2* can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, the yeast alpha-factor secretory signal/leader sequence, and linker sequences (if needed) for expression of vertebrate *patched-2*.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant vertebrate *patched-2* can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing vertebrate *patched-2* may further be purified using selected column chromatography resins.

Example 5

Expression of vertebrate *patched-2* in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of vertebrate *patched-2* in Baculovirus-infected insect cells.

5 The vertebrate *patched-2* is patched-2 upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the vertebrate *patched-2* or the desired portion of the vertebrate *patched-2* (such as the sequence encoding the extracellular domain of a transmembrane protein) is
10 amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin
15 (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression is performed as described by O'Reilley et al., Baculovirus expression vectors: A laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged vertebrate *patched-2* can then be purified, for example, by Ni²⁺-chelate
20 affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% Glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% Glycerol, pH 7.8)
25 and filtered through a 0.45 µm filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% Glycerol, pH 6.0), which elutes
30 nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged vertebrate *patched-2* are pooled and dialyzed against loading buffer.

35 Alternatively, purification of the IgG tagged (or Fc tagged) vertebrate *patched-2* can be performed using known chromatography techniques, including for instance, Protein A or protein G column

chromatography

Example 6

Preparation of Antibodies that Bind Vertebrate *patched-2*

This example illustrates preparation of monoclonal antibodies, which can specifically bind vertebrate *patched-2*.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, *supra*. Immunogens that may be employed include purified vertebrate *patched-2*, fusion proteins containing vertebrate *patched-2*, and cells expressing recombinant vertebrate *patched-2* on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the vertebrate *patched-2* immunogen (e.g., extracellular portions or cells expressed *patch-2*) emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect vertebrate *patched-2* antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of vertebrate *patched-2*. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-*patched-2* cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against vertebrate *patched-2*. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against vertebrate *patched-2* is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-vertebrate *patched-2* monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

Example 7

Gli Luciferase Assay

The following assay may be used to measure the activation of the transcription factor *GLI*, the mammalian homologue of the *Drosophila cubitus interruptus* (Ci). It has been shown that *GLI* is a transcription factor activated upon *SHh* stimulation of cells.

Nine (9) copies of a *GLI* binding site present in the HNF3 β enhancer. (Sasaki *et al.*, *Development*

124: 1313-1322 (1997)), are introduced in front of a thymidine kinase minimal promoter driving the luciferase reporter gene in the pGL3 plasmid (Promega). The sequence of the *GLI* binding sequence is: TCGACAAGCAGGGAACACCCAAGTAGAAGCTC (p9XGliLuc) (SEQ ID NO:31), while the negative control sequence is: TCGACAAGCAGGGAAGTGGGAAGTAGAAGCTC (p9XmGliLuc) (SEQ ID NO:32). These constructs are cotransfected with the full length *Ptch-2* and *Smo* in C3H10T1/2 cells grown in F12, DMEM (50:50), 10% FCS heat inactivated. The day before transfection 1×10^5 cells per well was inoculated in 6 well plates, in 2 ml of media. The following day, 1 μ g of each construct is cotransfected in duplicate with 0.025 mg ptkRenilla luciferase plasmid using lipofectamine (Gibco-BRL) in 100 μ l OptiMem (with GlutaMAX) as per manufacturer's instructions for 3 hours at 37°C. Serum (20%, 1 ml) is then added to each well and the cells were incubated for 3 more hours at 37°C. Cells are then washed twice with PBS, then incubated for 48 hours at 37°C in 2 ml of media. Each well is then washed with PBS, and the cells lysed in 0.5 ml Passive Lysis Buffer (Promega) for 15 min. at room temperature on a shaker. The lysate is transferred in eppendorf tubes on ice, spun in a refrigerated centrifuge for 30 seconds and the supernatant saved on ice. For each measure, 20 μ l of cell lysate is added to 100 μ l of LARII (luciferase assay reagent, Promega) in a polypropylene tube and the luciferase light activity measured. The reaction is stopped by the addition of Stop and Glow buffer (Promega), mixed by pipetting up and down 3 to 5 times and *Renilla* luciferase lights activity is measured on the luminometer.

Deposit of Material

The following materials have been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, USA (ATCC):

<u>Designation:</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
pRK7.hptc2.Flag-1405	209778	4/14/98

This deposit was made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposit will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to

practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable
5 the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

What is claimed is:

1. Isolated nucleic acid comprising DNA having at least a 95% sequence identity to (a) a DNA molecule encoding a *patched-2* polypeptide comprising the sequence of amino acids 1 to about 1203 of Fig. 1 (SEQ ID NO:2), or (b) the complement of (a); and encoding a polypeptide having *patched-2* biological activity.
2. An isolated nucleic acid comprising DNA having at least a 95% sequence identity to (a) a DNA molecule encoding the same mature polypeptide encoded by the cDNA in ATCC Deposit No. 209778 (designation: pRK7.hptc2.Flag-1405), or (b) the complement of the DNA molecule of (a).
3. (Amended) The isolated nucleic acid of claim 2 comprising human *patched-2* encoding sequence of the cDNA in ATCC deposit No. 209778 (designation: pRK7.hptc2.Flag-1405), or a sequence which hybridizes thereto under stringent conditions.
4. A vector comprising the nucleic acid of claim 1.
5. The vector of claim 4 operably linked to control sequences recognized by a host cell transformed with the vector.
6. A host cell transformed with the vector of claim 4.
7. The host cell of claim 6 which is mammalian.
8. The host cell of claim 7 wherein said cell is a CHO cell.
9. The host cell of claim 6 which is prokaryotic.
10. The host cell of claim 9 wherein said cell is an *E. coli*.
11. The host cell of claim 7 wherein said cell is a yeast cell.
12. The host cell of claim 11 which is *Saccharomyces cerevisiae*.
13. A process for producing *patched-2* polypeptides comprising culturing the host cell of claim 9 under conditions suitable for expression of vertebrate *patched-2* and recovering *patched-2* from the cell culture.
14. (Amended) Isolated native sequence human *patched-2* polypeptide comprising amino acid residues

1 to 1203 of Fig. 1 (SEQ ID NO:2).

15. (Amended) Isolated native sequence human *patched-2* polypeptide encoded by the nucleotide deposited under accession number ATCC 209778 (Designation: pRK7.hptc2.Flag-1405) having *patched-2* biological activity.

16. A chimeric molecule comprising vertebrate *patched-2* polypeptide *patched-2* to a heterologous amino acid sequence.

17. The chimeric molecule of claim 16 wherein said heterologous amino acid sequence is an epitope tag sequence.

18. The chimeric molecule of claim 17 wherein said heterologous amino acid sequence is a constant region of an immunoglobulin.

19. An antagonist of *patched-2* which blocks, prevents, inhibits and/or neutralizes the *Dhh* function in the *Dhh* signaling pathway.

20. The antagonist of claim 19 which is a small bioorganic molecule.

21. The antagonist of claim 19 which is an antisense nucleotide.

22. An agonist of *patched-2* which stimulates or enhances the normal functioning of *patched-2* in the *Dhh* signaling pathway.

23. (Amended) The agonist of claim 22 which prevents *Smo* (SEQ ID NO:17) inactivation of *ptch-2* (SEQ ID NO:2)

24. The agonist of claim 22 which is a small bioorganic molecule.

25. The agonist of claim 24 which is a small bioorganic molecule.

26. A method of screening for antagonists or agonists of *patched-2* biological activity comprising:

- (a) exposing *patched-2* expressing target cells in culture to a candidate compound and *Dhh*; and
- (b) analyzing cells for binding of *Dhh* to *patched-2*; or
- (c) scoring phenotypic or functional changes in the treated cells;

and comparing the results to control cells which were not exposed to the candidate compound.

27. A method of screening for antagonist or agonist molecule of *patched-2* biological activity comprising:

(a) exposing a *patched-2* ligand and a compound having *patched-2* biological activity to a candidate antagonist or agonist; and

5 (b) analyzing the substrate for binding of the ligand to the compound; and
comparing the results to control reactions which were not exposed to the candidate molecule.

28. A method of diagnosing to determine whether a particular disorder is modulated by *Dhh* signaling, comprising:

10 (a) culturing test cells or tissues;

(b) administering a compound which can inhibit *patched-2* modulated *Dhh* signaling; and

(c) analyzing the level of *Dhh* binding to *patched-2* or *Dhh* mediated phenotypic effects in the test cells.

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1 GTTATTTCAG GCCATGGTGT TCGCGCGAAT TAATTCCCGA TCCAGACATG ATAAGATACA TTGATGAGTT TGGACAAACC ACAACTAGAA TGCAGTGAAA
CAATAAAGTC CGGTACCACA ACGCGGCTTA ATTAAGGGCT AGGTCTGTAC TATTCTATGT AACTACTCAA ACCTGTTGG TGTGATCTT ACGTCACTTT
(SEQ ID NO: 1)

101 AAAATGCTTT ATTGTGAAA TTGTGATGC TATTGCTTTA TTTGTAACCA TTATAAGCTG CAATAACAA GTTGGGCCAT GCGGCCAAG CTTCTGCAGG
TTTTACGAAA TAAACACTTT AAACACTACG ATAACGAAAT AAACATTGGT AATATTCGAC GTTATTGTT CAACCCGGTA CCGCCGGTTC GAAGACGTCC

201 TCGACTCTAG AGGATCCCCG GGGAATTCCG GCATGACTCG ATCGCCGCC CTAAGAGAGC TGCCCCCGAG TTACACACCC CCAGCTCGAA CCGCAGCACC
AGCTGAGATC TCCTAGGGGC CCCTTAAGGC CGTACTGAGC TAGCGGCGGG GAGTCTCTCG ACGGGGCTC AATGTGTGGG GGTCGAGCTT GCGGTCGTGG
M T R S P P L R E L P P S Y T P P A R T A A P
1 ^insert starts here (SEQ ID NO: 2)

301 CCAGATCCTA GCTGGGAGCC TGAAGGCTCC ACTCTGGCTT CGTGCTTACT TCCAGGGCCT GCTCTTCTCT CTGGGATGCG GGATCCAGAG ACATTGTGGC
GGCTAGGAT CGACCTCGG ACTTCGAGG TGAGACCGAA GCACGAATGA AGGTCCCGGA CGAGAAGAGA GACCCCTACGC CCTAGGTCTC TGTAACACCCG

24 Q I L A G S L K A P L W L R A Y F Q G L L F S L G C G I Q R H C G

401 AAAGTGCTCT TTCTGGGACT GTTGGCCTTT GGGGCCCTGG CATTAGGTCT CCGCATGGCC ATTATTGAGA CAAACTTGA ACAGCTCTGG GTAGAAGTGG
TTTCACGAGA AAGACCTGA CAACCGGAAA CCCCAGGACC GTAATCCAGA GCGTACCGG TAATAACTCT GTTTGAACCT TGTCGAGACC CATCTTCACC

57 K V L F L G L L A F G A L A L G L R M A I I E T N L E Q L W V E V G

501 GCAGCCGGGT GAGCCAGGAG CTGCATTACA CCAAGGAGAA GCTGGGGAG GAGGTGCTAT ACACCTCTCA GATGCTGATA CAGACCGCAC GCCAGGAGG
CGTCGGCCCC CTCGGTCTC GACGTAATGT GGTCTCTCTT CGACCCCTC CTCCGACGTA TGTGGAGAGT CTACGACTAT GTCTGGCGTG CCGTCTCTCC

91 S R V S Q E L H Y T K E K L G E E A A Y T S Q M L I Q T A R Q E G

601 AGAGAACATC CTCACACCCG AAGCACTGG CCTCCACCTC CAGGCAGCCC TCACTGCCAG TAAAGTCCAA GTATCACTCT ATGGGAAGTC CTGGGATTG
TCTCTGTAG GAGTGTGGC TTCGTGAACC GGAGGTGGAG GTCCGTCGG AGTGACGTC ATTCAGGT CATAGTGAGA TACCCTTCAG GACCCCTAAC

124 E N I L T P E A L G L H L Q A A L T A S K V Q V S L Y G K S W D L

701 AACAAAATCT GCTACAAGTC AGGAGTTCCC CTTATTGAA ATGGAATGAT TGAGTGGATG ATTGAGAAGC TGTTCCCGTG CGTGATCCTC ACCCCCCTCG
TTGTTTGA CGATGTTTCA TCCTCAAGG GAATAACTTT TACCTTACTA ACTCACCTAC TAACTCTTCG ACAAAAGGCAC GCACTAGGAG TGGGGGAGC

157 N K I C Y K S G V P L I E N G M I E W M I E K L F P C V I L T P L D

801 ACTGCTTCTG GGAGGGAGCC AAATCCCAAG GGGGCTCCGC CTACCTGCC CTACCTGCCG ATATCCAGTG GACCAACCTG GATCCAGAGC AGTGTCTGA
TGACGAAGAC CCTCCCTCGG TTTGAGGTTT CCGGAGGCG GATGGACGGG CCGGGGGCC TATAGTCTAC CTGGTTGGAC CTAGGTCTCG TCGACGACCT

191 C F W E G A K L Q G G S A Y L P G R P D I Q W T N L D P E Q L L E

FIG. 1A

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901 GGAGCTGGGT CCCTTTGCCT CCCTTGAGGG CTTCGGGGAG CTGCTAGACA AGGCACAGGT GGGCCAGGCC TACGTGGGGC GGCCCTGTCT GCACCCTGAT
CCTCGACCCA GGGAAACGGA GGAAGTCCC GAAGGCCCTC GACGATCTGT TCCGTGTCCA CCGGTCCGG ATGCACCCCG CCGGACAGA CGTGGGACTA
224 E L G P F A S L E G F R E L L D K A Q V G Q A Y V G R P C L H P D

1001 GACCTCCACT GCCACCTAG TCCCCCAAC CATCACAGCA GGCAGGCTCC CAATGTGGCT CACGAGCTGA GTGGGGGCTG CCATGGCTTC TCCACAAAT
CTGGAGGTGA CCGGTGGATC ACGGGGTG GTAGTGTCT CCGTCCGAGG GTTACACCGA GTGCTCGACT CACCCCGGAC GGTACCCGAAG AGGTGTGTTA
257 D L H C P P S A P N H H S R Q A P N V A H E L S G G C H G F S H K F

1101 TCATGCACTG GCAGGAGGAA TTGCTGCTGG GAGGATGGC CAGAGACCCC CAAGGAGAGC TGCTGAGGGC AGAGGCCCTG CAGAGCACCT TCTTGCTGAT
AGTACGTGAC CGTCCCTCCTT AACGACGACC CTCCGTACCG GTCTCTGGG GTTCCTCTCG ACGACTCCC GTCCGGGAC GTCTCGTGA AGACGACTA
291 M H W Q E E L L L G G M A R D P Q G E L L R A E A L Q S T F L L M

1201 GAGTCCCCGC CAGCTGTACG AGCATTTCCG GGGTGACTAT CAGACACATG ACATTGGCTG GAGTGAGGAG CAGGCCAGCA CAGTGCTACA AGCCTGGCAG
CTCAGGGCG GTGACATGC TCGTAAAGC CCCACTGATA GTCTGTGTAC TGTAACCGAC CTCACTCCTC GTCCGGTCTG GTCACGATGT TCGGACCGTC
324 S P R Q L Y E H F R G D Y Q T H D I G W S E E Q A S T V L Q A W Q

1301 CGGCGCTTG TGCAGCTGGC CCAGGAGGCC CTGCCCTGAGA ACGCTTCCCA GCAGATCCAT GCCTTCTCCT CCACCACCCT GGATGACATC CTGCATGCGT
GCCGCGAAC ACGTCGACCG GGTCTCTCCG GACGACTCT TCGGAAGGT TGCCTAGTA CGGAAGAGGA GGTGGTGGG CCTACTGTAG GACGTACGCA
357 R R F V Q L A Q E A L P E N A S Q Q I H A F S S T T L D D I L H A F

1401 TCTCTGAAGT CAGTGCTGCC CGTGTGGTGG GAGGTATCT GCTCATGCTG GCCTATGCCT GTGTGACCAT GCTGGGGTGG GACTGCGCC AGTCCCAGGG
AGAGACTTCA GTCACGACGG GCACACCCACC CTCCGATAGA CGAGTACGAC CGGATACGGA CACACTGGTA CGACGCCACC CTGACGCGGG TCAGGGTCCC
391 S E V S A A R V V G G Y L L M L A Y A C V T M L R W D C A Q S Q G

1501 TTCCGTGGGC CTTGCCGGGG TACTGCTGGT GGCCTGGCG GTGGCCTCAG GCCTTGGGCT CTGTGCCCTG CTCGGCATCA CCTTCAATGC TGCCACTACC
AAGGCACCCG GAACGGCCCC ATGACGACCA CCGGACCCG CACCGAGTC CGGAACCCGA GACACGGGAC GAGCCGTAGT GGAAGTTAG ACGGTGATGG
424 S V G L A G V L L V A L A V A S G L G L C A L L G I T F N A A T T

1601 CAGGTGCTGC CTTTCTTGGC TCTGGGAATC GCGTGGATG ACGTATTCCT GCTGGCGCAT GCCTTCACAG AGGCTCTGCC TGGCACCCCT CTCCAGGAGC
GTCCACGACG GAAAGAACC AGACCCCTAG CCGCACCTAC TGCATAAGGA CGACCCGTA CGGAAGTGT CCGAGACCG ACCGTGGGA GAGGTCTCTG
457 Q V L P F L A L G I G V D D V F L L A H A F T E A L P G T P L Q E R

1701 GCATGGGCGA GTGTCTGCAG CGCAGGGGA CCAGTGTCT ACTCACATCC ATCAACAACA TGGCCGCCCTT CCTCATGGCT GCCCTCGTTC CCATCCCTGC
CGTACCCGCT CACAGACGTC GCGTGCCCGT GGTCACAGCA TAGTGTAGG TAGTTGTGT ACCGGCGGA GGAGTACCGA CCGGAGCAAG GGTAGGACG
491 M G E C L Q R T G T S V V L T S I N N M A A F L M A A L V P I P A

FIG. 1B

1801 GCTGCGAGCC TTCTCCCTAC AGGCGGCCAT AGTGGTTGGC TGCACCTTTG TAGCCGTGAT GCTTGCTTTC CCAGCCATCC TCAGCCTGGA CCTACGGCGG
CGACGCTCGG AAGAGGGATG TCCGCCGGTA TCACCAACCG ACGTGAAC ATCGGCACTA CGAACAGAAG GGTGGTAGG AGTCGGACCT GGATGCCGCC
524 L R A F S L Q A A I V V G C T F V A V M L V F P A I L S L D L R R
1901 CGCCACTGCC AGCGCCTTGA TGTGCTCTGC TGCTTCTCCA GTCCCTGCTC TGCTCAGGTG ATTCAGATCC TGCCCCAGGA GCTGGGGGAC GGGACAGTAC
GCGGTGACCG TCGCGGAAC ACACGAGACG ACGAAGAGGT CAGGACGAG ACGAGTCCAC TAAGTCTAGG ACGGGTCTCT CGACCCCTCTG CCTGTGTCATG
557 R H C Q R L D V L C C F S S P C S A Q V I Q I L P Q E L G D G T V P
2001 CAGTGGGCAT TGCCACCTC ACTGCCACAG TTCAAGCCTT TACCCACTGT GAAGCCAGCA GCCAGCATGT GGTACCATC CTGECTCCCC AAGCCACCT
GTCACCCGTA ACGGGTGGAG TGACGGGTGC AAGTTCGGAA ATGGGTGACA CTTCGGTCTG CCGTCGTACA CCAGTGTAG GACGGAGGGG TTCGGGTGGA
591 V G I A H L T A T V Q A F T H C E A S S Q H V V T I L P P Q A H L
2101 GGTGCCCCCA CCTTCTGACC CACTGGGCTC TGAGCTCTTC AGCCCTGGAG GTTCCACACG GGACCTTCTA GGCCAGGAGG AGGAGACAAG GCAGAAGGCA
CCACGGGGT GGAAGACTGG GTGACCCGAG ACTCGAGAAG TCGGACCTC CCAGGTGTGC CCTGGAAGAT CCGGTCTCTC TCCTCTGTTC CGTCTTCCGT
624 V P P P S D P L G S E L F S P G G S T R D L L G Q E E T R Q K A
2201 GCCTGCAAGT CCCTGGGCTG TGCCGGCTGG AATCTTGCCC ATTTGCCCC CTATCAGTTT GCCCGGTGTC TGCTCCAGTC ACATGCCAAG GCCATCGTGC
CGGACGTTCA GGGACGGGAC ACGGGCGACC TTAGAACGGG TAAAGCGGC GATAGTCAA CGGGCAACG ACGAGGTGAG TGTACGGTTC CGGTAGCACG
657 A C K S L P C A R W N L A H F A R Y Q F A P L L L Q S H A K A I V L
2301 TGGTGCTCTT TGGTGCTCTT CTGGGCTGA GCCTCTACGG AGCCACCTTG GTGCAAGACG GCCTGGCCCT GACGGATGTG GTGCCCTCGG GCACCAAGGA
ACCACGAGAA ACCACGAGAA GACCGGACT GCGGTGGAAC CACGTTCTGC CGGACCGGGA CTGCTTACAC CACGGAGCCC CGTGGTTCTT
691 V L F G A L L G L S L Y G A T L V Q D G L A L T D V V P R G T K E
2401 GCATGCCCTC CTGAGCGGCC AGCTCAGGTA CTTCTCCCTG TACGAGGTG CCCTGGTGAC CCAGGGTGGC TTTGACTAGC CCCATTCCCA ACGCGCCCTC
CGTACGGAAG GACTCGCGG TCGAGTCCAT GAAGAGGGAC ATGCTCCACC GGGACCACTG GGTCCACCG AACTGATGC GGTAAAGGT TCGCGGGGAG
724 H A F L S A Q L R Y F S L Y E V A L V T Q G G F D Y A H S Q R A L
2501 TTTGATCTGC ACCAGCGCT CAGTCCCTC AAGCGGTGC TGCCCCACC GGCACCCAG GCACCCCGCA CCTGGCTGCA CTATTACCGC AACTGGCTAC
AAACTAGACG TGGTCGGAA GTCAAGGGAG TTCCGCCACG ACGGGGTG CCGGTGGTC CGTGGGCGT GGACCGACGT GATAATGGCG TTGACCGATG
757 F D L H Q R F S S L K A V L P P P A T Q A P R T W L H Y Y R N W L Q
2601 AGGGAATCCA GGCTGCCTT GACCAGGACT GGGCTTCTGG GCGCATCACC CGCCACTCGT ACCGCAATGG CTCTGAGGAT GGGGCCCTGG CCTACAAGCT
TCCCTTAGT CCGACGGAA CTGGTCTGA CCCGAAGACC CCGGTAGTG GCGGTAGCA TGGCGTTACC GAGACTCCTA CCGCGGACC GGATGTTTGA
791 G I Q A A F D Q D W A S G R I T R H S Y R N G S E D G A L A Y K L

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FIG. 1C

2701 GCTCATCCAG ACTGGAGACG CCCAGGAGCC TCTGGATTTC AGCCAGCTGA CCACAAGGAA GCTGGTGGAC AGAGAGGGAC TGATTCCACC CGAGCTCTTC
CGAGTAGGTC TGACCTCAGC GGGTCCCTCGG AGACCTAAG TCGGTGCACT GGTGTTCTT CGACCACCTG TCTCTCCCTG ACTAAGGTGG GCTCGAGAAG
824 L I Q T G D A Q E P L D F S Q L T T R K L V D R E G L I P P E L F

2801 TACATGGGC TGACCGGTG GGTAGCAGT GACCCCTGG GTCTGGCAGC CTCACAGGC AACTTCTACC CCCACCTCC TGAATGGCTG CACGACAAAT
ATGTACCCCG ACTGGCACAC CCACTCGTCA CTGGGGGACC CAGACCGTCG GAGTGTCGG TTGAAGATGG GGGGTGGAGG ACTTACCGAC GTGCTGTTTA
857 Y M G L T V W V S S D P L G L A A S Q A N F Y P P P P E W L H D K Y

2901 ACGACACCAC GGGGGAGAAC CTTGCGATCC CGCCAGCTCA GCCCTTGGAG TTTGCCCAGT TCCCCTTCTT GCTGCGTGGC CTCCAGAAGA CTGCAGACTT
TGCTGTGGTG CCCCCTCTTG GAAGCGTAGG GCGGTGAGT CGGGAACCTC AAACGGGTCA AGGGGAAGGA CGACGCACCG GAGGTCTTCT GACGTCTGAA
891 D T T G E N L R I P P A Q P L E F A Q F P F L L R G L Q K T A D F

3001 TGTGAGGCC ATCGAGGGG CCCGGGCAGC ATGCGCAGAG GCCGGCCAGG CTGGGGTGCA CGCCTACCCC AGCGGCTCCC CTTCTCTCTT CTGGGAACAG
ACACCTCCCG TAGCTCCCCC GGGCCCGTCG TAGCGGTCTC CGGCCGTCC GACCCACCGT GCGGATGGG TCGCCGAGG GGAAGGAGAA GACCCCTGTC
924 V E A I E G A R A C A E A G Q A G V H A Y P S G S P F L F W E Q

3101 TATCTGGGC TCGGGCGCTG CTTCTGCTG GCGTCTGCA TCCTGCTGGT GTGCACCTTC CTGCTCTGTG CTCTGCTGCT CCTCAACCCC TGGACGGCTG
ATAGACCCCG ACGCCGCGAC GAAGGACGAC CGGCAGACGT AGGACGACCA CACGTGAAAG GAGCAGACAC GAGACGACGA GGAGTTGGG ACCTGCCGAC
957 Y L G L R R C F L L A V C I L L V C T F L V C A L L L L L N P W T A G

3201 GCCTCATAGT GCTGGTCCCTG GCGATGATGA CAGTGGAAC TTTGGTATC ATGGGTTTC TGGGCATCA GCTGAGTGCC ATCCCCGTGG TGATCCTTGT
CGGAGTATCA CGACCAGGAC CGTACTACT GTCACCTTGA GAAACCATAG TACCCAAAGG ACCCGTAGT CGACTCACCG TAGGGGCACC ACTAGGAACA
991 L I V L V L A M M T V E L F G I M G F L G I K L S A I P V V I L V

3301 GGCTCTGTA GGCATTGGG TTGATTAC AGTCCACGTG GCTCTGGCT TCCTGACCAC CCAGGGCAGC CGGAACCTGC GGGCCGCCCA TGCCCTTGAG
CCGAGACAT CCGTAACCGC AACTCAAGTG TCAGGTGCAC CGAGACCCGA AGGACTGGTG GTCCCGTCC GCTTGGAGC CCCGGCGGT ACGGAACTC
1024 A S V G I G V E F T V H V A L G F L T T Q G S R N L R A A H A L E

3401 CACACATTG CCCCCTGAC CGATGGGGC ATCTCCACAT TGCTGGGTCT GCTCATGCTT GCTGGTCCC ACTTTGACTT CATGTAAAG TACTTCTTG
GTGTGTAAC GGGGGCACTG GCTACCCCGG TAGAGGTGA ACGACCCAGA CGAGTACGAA CGACCAAGG TGAACACTGAA GTAACATTCC ATGAAGAAAC
1057 H T F A P V T D G A I S T L L G L L M L A G S H F D F I V R Y F F A

3501 CGGCGCTGAC AGTGCTCAG CTCCTGGGC TCCTCCATGG ACTCGTGCTG CTGCCTGTGC TGCTGTCCAT CCTGGGCCCG CCGCCAGAGG TGATACAGAT
GCCGCGACTG TCACGAGTGC GAGGACCCCG AGGAGGTACC TGAGCACGAC GACGGACAGC ACGACAGGTA GGACCCGGG GCGGTCTCC ACTATGTCTA
1091 A L T V L T L L G L L H G L V L L P V L L S I L G P P P E V I Q M

FIG. 1D

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3601 GTACAAGGAA AGCCAGAGAGA TCCTGAGTCC ACCAGCTCCA CAGGAGGCG GGCTTAGGTG GGGGCATCC TCCTCCCTGC CCCAGAGCTT TGCCAGAGTG
CATGTTCTT TCGGGTCTCT AGGACTCAGG TGGTCGAGGT GTCCCTCCGC CCGAATCCAC CCCCCTAGG AGGAGGACG GGGTCTCGAA ACGGTCTCAC
1124 Y K E S P E I L S P P A P Q G G G L R W G A S S S L P Q S F A R V
3701 ACTACCTCCA TGACCGTGGC CATCCACCCA CCCCCCTGC CTGGTGCCTA CATCCATCCA GCCCCTGATG AGCCCCCTTG GTCCCCCTGCT GCCACTAGCT
TGATGGAGGT ACTGGACCG GTAGGTGGGT GGGGGGACG GACCACGGAT GTAGGTAGGT CCGGGGGAAC CAGGGGACGA CCGTGATCGA
1157 T T S M T V A I H P P P L P P A Y I H P A P D E P P W S P A A T S S
3801 CTGGCAACCT CAGTTCCAGG GGACCAAGTC CAGCCACTGG GTGAAGAGC AGCTGAAGCA CAGAGACCAT GTGTGGGGCG TGTGGGGTCA CTGGGAAGCA
GACCGTTGGA GTCAGGTCC CCTGGTCCAG GTCGGTGACC CACTTCTCG TCGACTTCGT GTCTCTGGTA CACACCCCGC ACACCCCACT GACCCCTTCGT
1191 G N L S S R G P G P A T G O 1203
3901 CTGGGTCTGG TGTTAGACGC AGGACGGACC CCTGGAGGC CCTGCTGCTG CTGCATCCCC TCTCCCGACC CAGCTGTCTAT GGGCCTCCCT GATATCGAAT
GACCCAGACC ACAATCTGCG TCCTGCCTGG GGACCTCCCG GGACGACGAC GACGTAGGGG AGAGGGCTGG GTCGACAGTA CCCGGAGGGA CTATAGCTTA
^T to C (silent) PRK follows, this is the 5prime end of vector^
4001 TCAATCGATA GAACCGAGGT GCAGTTGGAC
AGTTAGCTAT CTTGGCTCCA CGTCAACCTG

FIG. 1E

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(SEQ ID NO: 3)

	30	40	50	60	70
905531	GCTGGGGTGCACGCCTACCNACAGCGGNTCCCCCTTCCTCTTCTGCGGAACA				
	:::	::	:	*****	*****
hpatched	CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGCGGAGCA				

(SEQ ID NO: 4)

	3010	3020	3030	3040	3050
905531	GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGG				
	***	*	*****	**	*
hpatched	GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTTCATCAGCGTGGTGTGG				

	3060	3070	3080	3090	3100
905531	TGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTNAACCCCTGGACGGCT				
	*****	*****	**	***	*
hpatched	CCTGCACATTCCTCGTGTGCGCTGTCTTCCTTCTGAACCCCTGGACGGCC				

	3110	3120	3130	3140	3150
905531	GGCCTNATAGTGCTGGTCCTGGCGATGATGACAGTGGAACCTTTGGTAT				
	**	*****	***	*****	*****
hpatched	GGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTGTTCCGGCAT				

	3160	3170	3180	3190	3200
905531	CATGGGTTTNCCTGGGCATCAAGCTGAGT				
	*****	**	*	**	*****
hpatched	GATGGGCCTCATCGGAATCAAGCTCAGT				

	3210	3220	3230		
905531	TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGT				
	:::	:::	*	**	*
hpatched	GCTGCTGCTGTTTCATCAGCGTGGTGTGGCC---TGCACATTCCTCGTGT				

	3090	3100	3110	3120	
905531	GCACTTTCCTCGTCTGTGCTCTGCTGCT				
	**	**	**	**	*
hpatched	GCGCTGTCTTCCTTCTGAACCCCTGGAC				

	3130	3140	3150		
--	------	------	------	--	--

FIG. 2A

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(SEQ ID NO: 5) 1326258 30 40 50 60 70
GCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGCGAACA
::: :: : *****
hpatched 3010 3020 3030 3040 3050
CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGCGGAGCA
1326258 80 90 100 110 120
GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGG
*** * ***** * * * * *
hpatched 3060 3070 3080 3090 3100
GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTTCATCAGCGTGGTGTGG
1326258 130 140 150
TGTGCACTTTCCTCNTCTGTGCTCT

hpatched 3110 3120 3130
CCTGCACATTCCTCGTGTGCGCTGT

1326258 90 100 110 120 130
TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGT
::: ::: * * * * *
hpatched 3090 3100 3110 3120
GCTGCTGCTGTTTCATCAGCGTGGTGTGGCC---TGCACATTCCTCGTGT
1326258 140 150
GCACTTTCCTCNTCTGTGCTCT
* * * * *
hpatched 3130 3140
GCGCTGTCTTCCTTCTGAACCC

1326258 10 20 30 40 50
CCGGGCAGCATGCGCAGAGGCCGGCCAGGCTGGGGTGCACGCCTACCCCA

(SEQ ID NO: 6) hpatched.RC 710 720 730 740 750
CCGGGCGGCATG--GCGAAGCGGACCAAGCTGGGGGGTGGCTCAGGGGAG

FIG. 2B

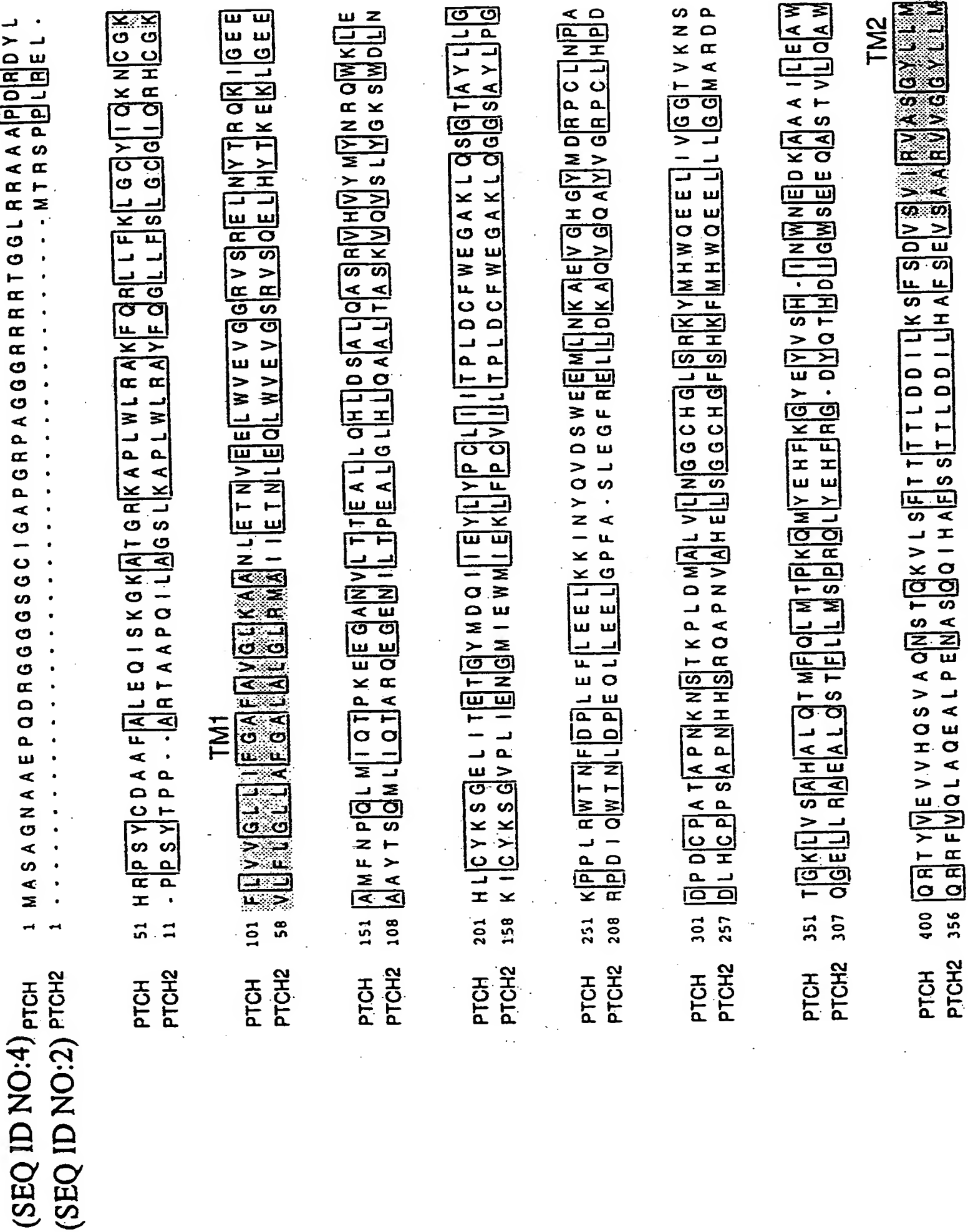


FIG. 3A

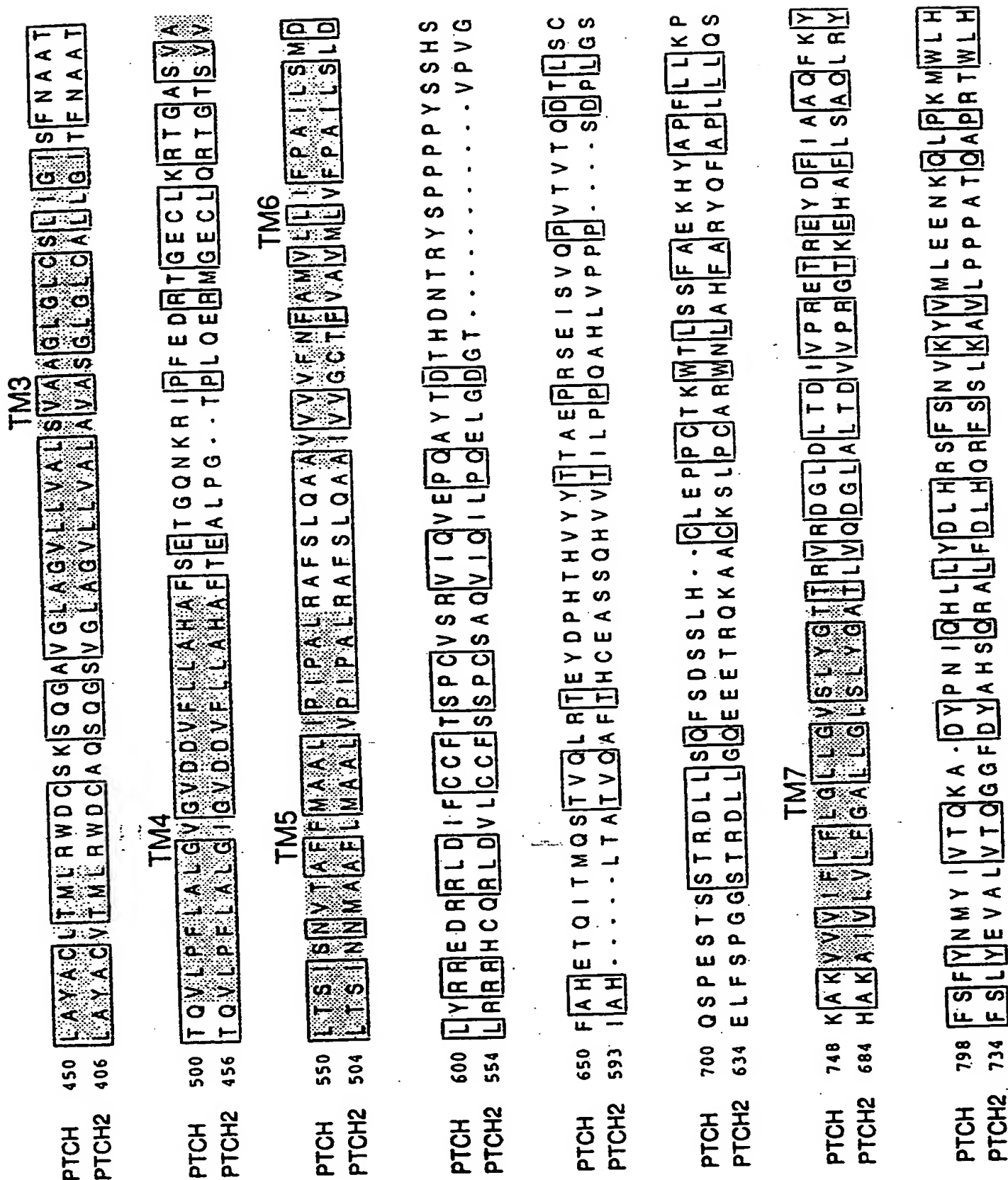


FIG. 3B

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FIG. 3C

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PTCH 1247 AGGPAHQVIVEATENPVFAHSTVHPESRHHPPSNPRQQPHLDSGSLPPG
PTCH2 1182 PWSPAATSSGNLSSRGPGPATG
PTCH 1297 RQGQPRRDPPREGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARS
PTCH 1347 HNPRNPASTAMGSSVPGYCQPIITTTASASVTVAVHPPVPVGPGRNPRGG
PTCH 1397 LCPGYPETHGLFEDPHVPPFHVRCERRDSKVEVIELQDVECEEERPRGSSS
PTCH 1447 N

FIG. 3D

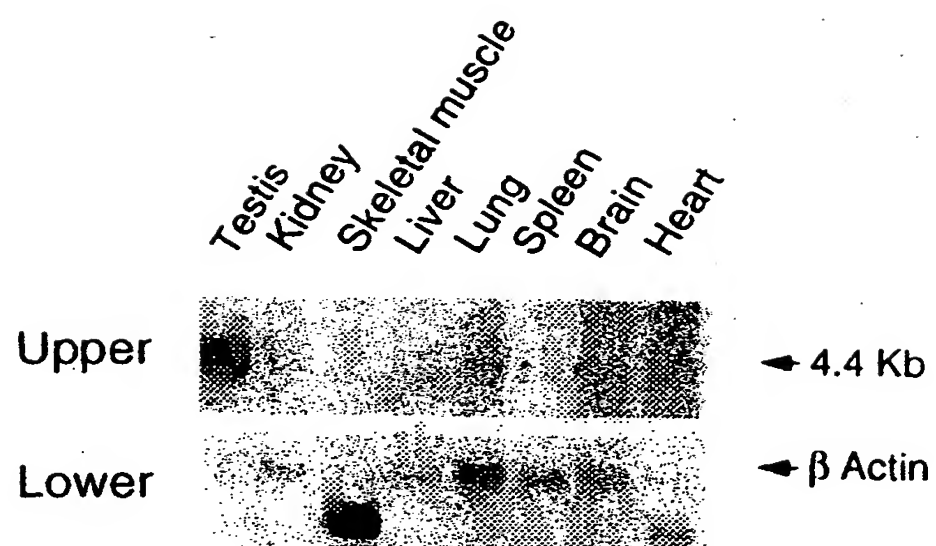


FIG. 4

SUBSTITUTE SHEET (RULE 26)

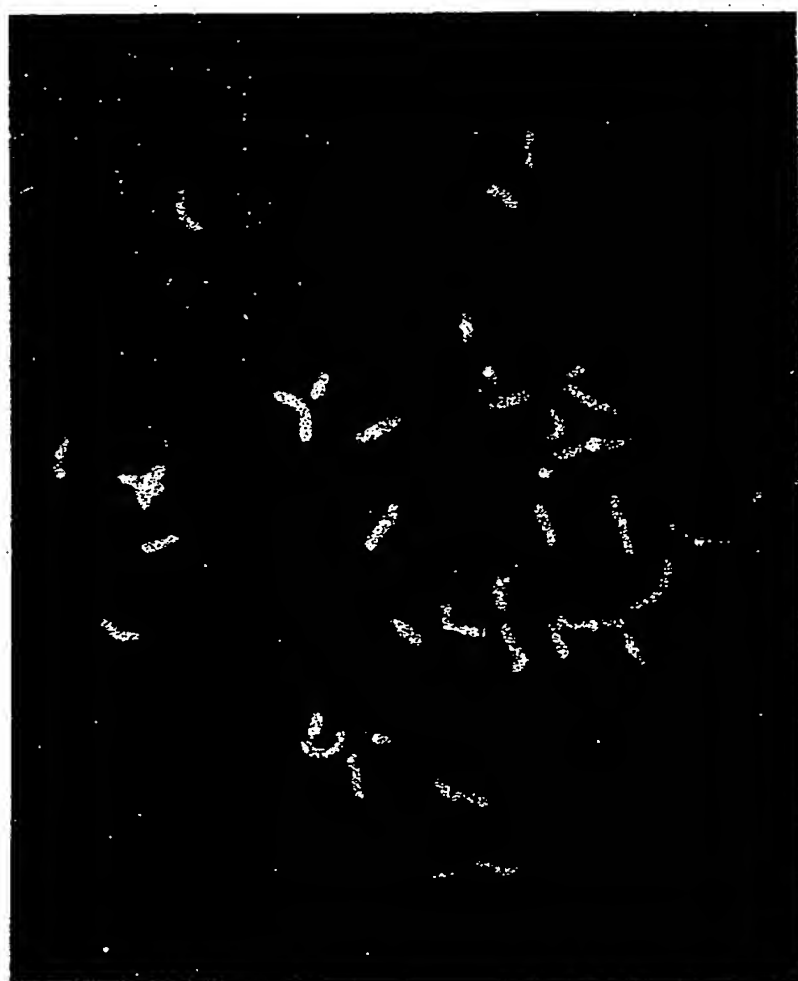


FIG. 5

SUBSTITUTE SHEET (RULE 26)



FIG. 6C



FIG. 6B

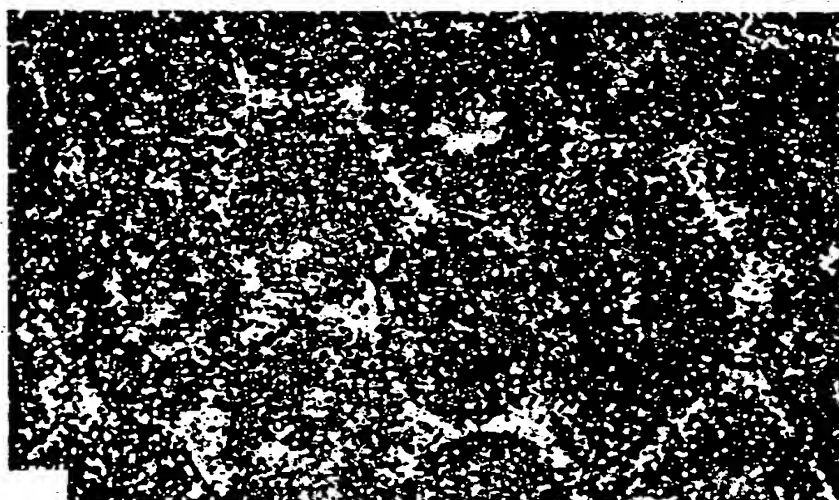


FIG. 6A



FIG. 6F

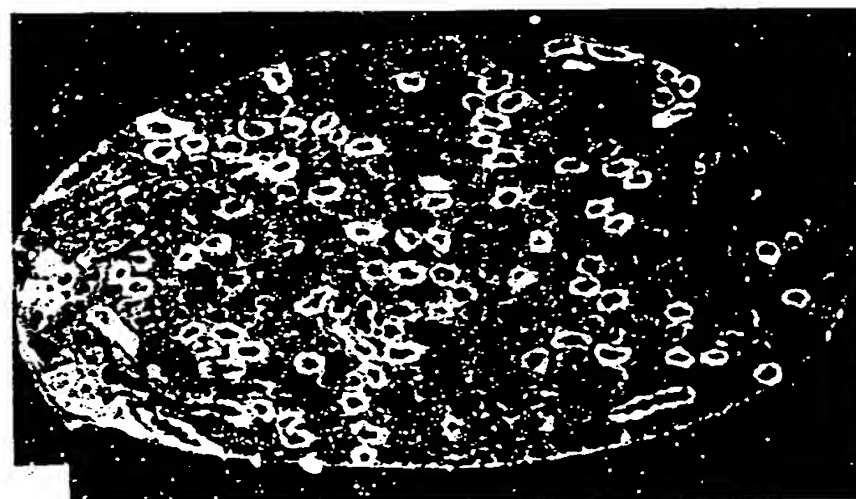


FIG. 6E



FIG. 6D

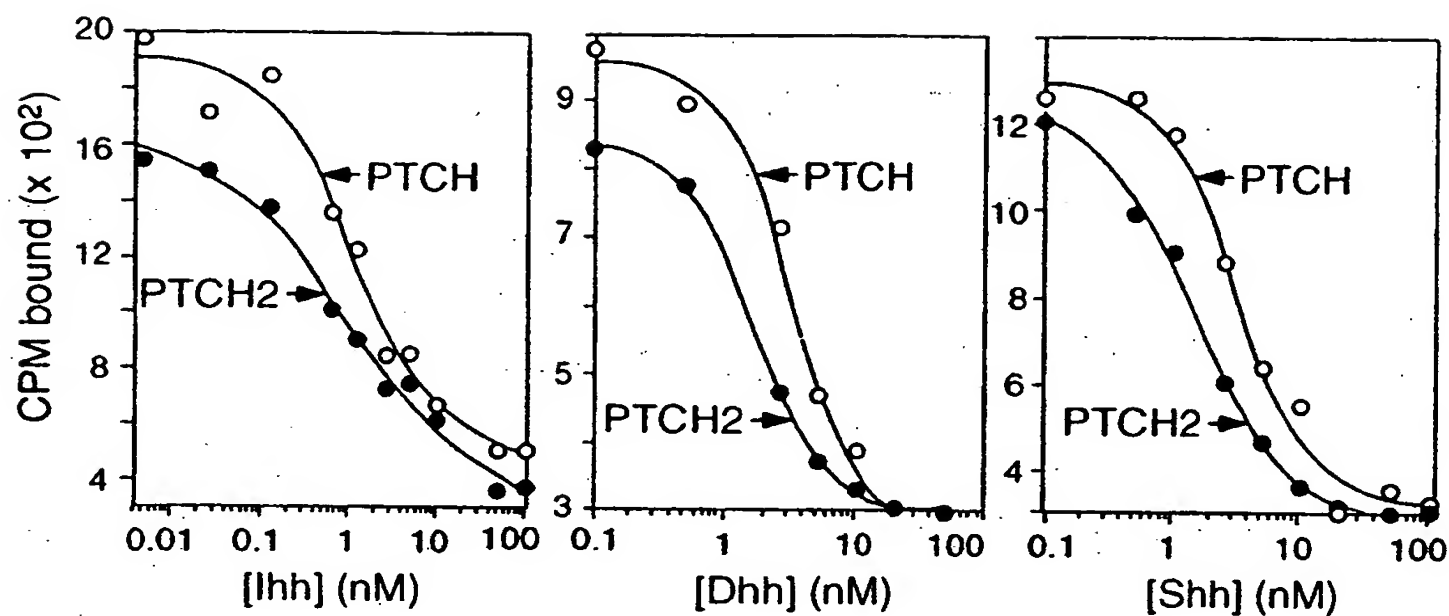


FIG. 7A

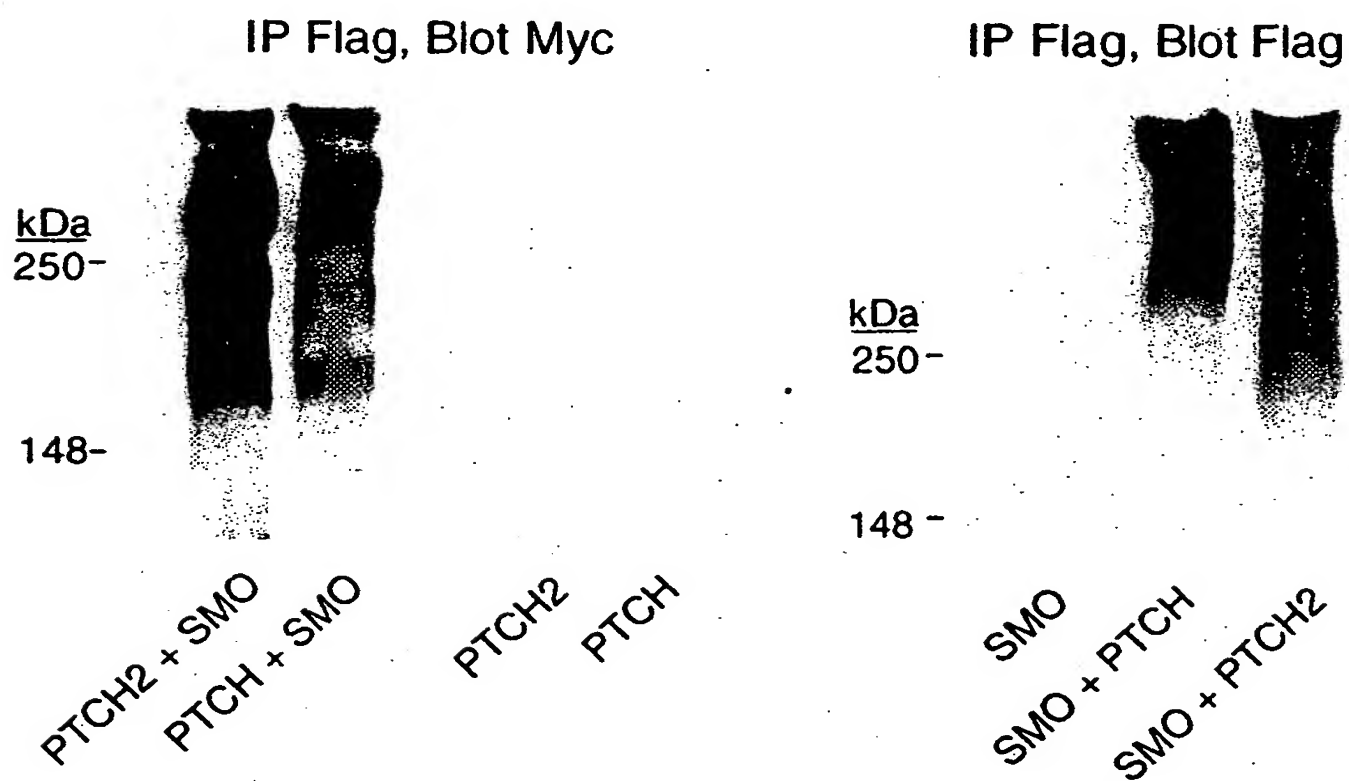


FIG. 7B

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	10	20	30	40	50
<i>hPtch-2</i>	MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCG				
	* * . * ***** . *** . ***** . ***** . *****				
<i>mPatched2</i>	MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCR				
(SEQ ID NO:7)	10	20	30	40	50
	60	70	80	90	100
<i>hPtch-2</i>	IQRHCGKVLFLGLLAFGALALGLRMAI IETNLEQLWVEVGSRVSQELHYT				
	** . ***** . ***** . * . *** . ***** . *****				
<i>mPatched2</i>	IQKHCGKVLFLGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYT				
	60	70	80	90	100
	110	120	130	140	150
<i>hPtch-2</i>	KEKLGEEAAYTSQMLIQATARQEGENILTPEALGLHLQAALTASKVQVSLY				
	***** . ***** . *** * . ***** . ***** . *****				
<i>mPatched2</i>	KEKLGEEAAYTSQMLIQTAHQEGGNVLTPEALDLHLQAALTASKVQVSLY				
	110	120	130	140	150
	160	170	180	190	200
<i>hPtch-2</i>	GKSWDLNKICYKSGVPLIENGMIIEWMIEKLFPCVILTPLDCFWEGAKLQG				
	***** . ***** . ***** . ***** . *****				
<i>mPatched2</i>	GKSWDLNKICYKSGVPLIENGMIERMIEKLFPCVILTPLDCFWEGAKLQG				
	160	170	180	190	200
	210	220	230	240	250
<i>hPtch-2</i>	GSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELDDKAQVGQAYVGR				
	***** . ***** . ***** . ***** . *****				
<i>mPatched2</i>	GSAYLPGRPDIQWTNLDPPQLLEELGPFASLEGFRELDDKAQVGQAYVGR				
	210	220	230	240	250
	260	270	280	290	300
<i>hPtch-2</i>	PCLHPDDLHCPPSAPNHHSRQAPNVAHELSSGGCHGFSHKFMHWQEELLLG				
	*** . *** . ***** . ***** . ***** . ***** . *****				
<i>mPatched2</i>	PCLDPDDPHCPPSAPNRHSRQAPNVAQELSSGGCHGFSHKFMHWQEELLLG				
	260	270	280	290	300
	310	320	330	340	350
<i>hPtch-2</i>	GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQAST				
	* . *** . * . ***** . ***** . ***** . ***** . *****				
<i>mPatched2</i>	GTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASM				
	310	320	330	340	350

FIG. 8A

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	360	370	380	390	400
<i>hPtc-2</i>	VLQAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVG				

<i>mPatched2</i>	VLQAWQRRFVQLAQEALPANASQQIHAFSSTTLDDILRAFSEVSTTRVVG				
	360	370	380	390	400
	410	420	430	440	450
<i>hPtc-2</i>	GYLLMLAYACVTMLRWDCASQSGSVGLAGVLLVALAVASGLGLCALLGIT				

<i>mPatched2</i>	GYLLMLAYACVTMLRWDCASQSGAVGLAGVLLVALAVASGLGLCALLGIT				
	410	420	430	440	450
	460	470	480	490	500
<i>hPtc-2</i>	FNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGT				

<i>mPatched2</i>	FNAATTQVLPFLALGIGVDDIFLLAHAFKAPPDTPPLPERMGECLRSTGT				
	460	470	480	490	500
	510	520	530	540	550
<i>hPtc-2</i>	SVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAIL				
	** ***				
<i>mPatched2</i>	SVALTSVNNMVAFMAALVPIPALRAFSLQAAIVVGCNFAAVMLVFPAIL				
	510	520	530	540	550
	560	570	580	590	600
<i>hPtc-2</i>	SLDLRRRHCRQLDVLCCFSSPCSAQVIQILPQELGDGTVPVGGIAHLTATV				

<i>mPatched2</i>	SLDLRRRHRQLDVLCCFSSPCSAQVIQMLPQELGDRAVPVGGIAHLTATV				
	560	570	580	590	600
	610	620	630	640	650
<i>hPtc-2</i>	QAFTHCEASSQHVVITLPPQAHLPVPPSDPLGSELFSPGGSTRDLLGQEE				

<i>mPatched2</i>	QAFTHCEASSQHVVITLPPQAHLLSPASDPLGSELYSPGGSTRDLLSQEE				
	610	620	630	640	650
	660	670	680	690	700
<i>hPtc-2</i>	ETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLS				
	* .***. * ** * *****				
<i>mPatched2</i>	GTGPQAACRPLLCAHWTLAHFARYQFAPLLLQTRAKALVLLFFGALLGLS				
	660	670	680	690	700

FIG. 8B

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	710	720	730	740	750
<i>hPtc-2</i>	LYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYA				

<i>mPatched2</i>	LYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYA				
	710	720	730	740	750
	760	770	780	790	800
<i>hPtc-2</i>	HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYRNLQGIQAQAFDQDW				

<i>mPatched2</i>	HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYRNLQGIQAQAFDQDW				
	760	770	780	790	800
	810	820	830	840	850
<i>hPtc-2</i>	ASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVLDREGL				

<i>mPatched2</i>	ASGRITRHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLTTRKLVLDKEGL				
	810	820	830	840	850
	860	870	880	890	900
<i>hPtc-2</i>	IPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP				

<i>mPatched2</i>	IPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP				
	860	870	880	890	900
	910	920	930	940	950
<i>hPtc-2</i>	PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSP				

<i>mPatched2</i>	AAQPLEFAQFPFLLHGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSP				
	910	920	930	940	950
	960	970	980	990	1000
<i>hPtc-2</i>	FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMT				

<i>mPatched2</i>	FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLSPWTAGLIVLVLAMMT				
	960	970	980	990	1000
	1010	1020	1030	1040	1050
<i>hPtc-2</i>	VELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTSQGSRLNR				

<i>mPatched2</i>	VELFGIMGFLGIKLSAIPVVILVASIGIGVEFTVHVALGFLTSHGSRNLR				
	1010	1020	1030	1040	1050

FIG. 8C

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	1060	1070	1080	1090	1100
<i>hPtch-2</i>	AAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLGL				
	** ***.*****.*****.*****.*****.*****				
<i>mPatched2</i>	AASALEQTFAPVTDGAVSTLLGLLMLAGSNFDFIIRYFFVVLTVLTLGL				
	1060	1070	1080	1090	1100
	1110	1120	1130	1140	1150
<i>hPtch-2</i>	LHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGGLRWGASSLP				
	****.*****.*.*.*****.*...***.*****...*				
<i>mPatched2</i>	LHGLLLL PVLLSILGPPPQVVQVYKESPQTLNSAAPQRGGLRWDRPPTLP				
	1110	1120	1130	1140	1150
	1160	1170	1180	1190	1200
<i>hPtch-2</i>	QSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP				
	*****.*****.***.*				
<i>mPatched2</i>	QSFARVTTSMTVALHPPPLPGAYVHPASEEPT				
	1160	1170	1180		
<i>hPtch-2</i>	ATG				

FIG. 8D

PTCH2



PTCH



FIG. 9

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> C nsensus Sequence of human patched 2 cDNA clone
> length: 4004 bp

(SEQ ID NO:8)

1 CCCACGGGTC CCGGAGAAAGC TGGGGGAGGA GGTGTCATAC ACCTCTCAGA TGCTGATACA GACCGCACGC CAGGAGGAG AGAACATCCT CACACCCGAA
GGGTGCGCAG GCCCTCTTCG ACCCCCTCCT CCGACGTATG TGGAGAGTCT ACGACTATGT CTGGCGTGCG GTCCTCCCTC TCTTGTAGGA GTGTGGGCTT

race 6

101 GCACTTGGCC TCCACCTCCA GGCAGCCCTC ACTGCCAGTA AAGTCCAAAGT ATCACTCTAT GGAAGTCTT GGGATTGAA CAAAATCTGC TACAAGTCAG
CGTGAACCGG AGGTGGAGGT CCGTCGGGAG TGACGGTCAT TTCAGGTTCA TAGTGAGATA CCCTTCAGGA CCTTAACTT GTCCTTACG ATGTTTCAGTC

race 5

201 GAGTTCCCTT TATTGAAAT GGAATGATTG AGCGGATGAT TGAGAAGCTG TTTCCGTGCG TGATCCTCAC CCCCCTCGAC TGCTTCTGG AGGAGCCAA
CTCAAGGGGA ATAACTTTTA CCTTACTAAC TCGCCTACTA ACTCTTCGAC AAAGGCACGC ACTAGGAGTG GGGGAGCTG ACGAAGACCC TCCCTCGGTT

301 ACTCCAAGG GGTCCGCTT ACCTCCGCTT CCCAATGTGG CTCACGAGCT GAGTGGGGC TGCCATGGCT TCTCCCACAA ATTCAATGCAC TGGCAGGAGG
TGAGGTTCCC CCGAGGCGGA TGGACGGCGA GGGTTACACC GAGTGCTCGA CTCACCCCGG ACGGTACCGA AGAGGGTGT TAAATACGTG ACCGTCTCTC

401 AATTGCTGCT GGGAGGCATG GCCAGAGACC CCCAAGGAGA GCTGCTGAGG GCAGAGGCC TGACAGACAC CTTCCTGCTG ATGAGTCCCC GCCAGCTGTA
TTAACGACGA CCTCCGCTAC CGTCTCTG GGGTTCTCTT CGACGACTAC CTTCTCCGCT AGGTCTCTCT GAAGAACGAT TACTCAGGGG CCGTCCGACAT

501 CGAGCATTTT CCGGGTGACT ATCAGACACA TGACATTGGC TGGAGTGAGG AGCAGGCCAG CACAGTGCTA CAAGCCTGSC AGCGGCGCTT TGTGCAGGTC
GCTCGTAAAG GCCCCTACTGA TAGTCTGTGT ACTGTAAACG ACCTCACTCC TCGTCCGGTC GTGTACGAT GTTCGGACCG TCGCCGCGAA ACACGTCCAG

601 GGTATGGACA AGGACAGGG GGTGCCCTGA GGCCATTCCC TCCTCTGCTC CCCTCCTATC CACCTGTGTT CTCCAGCTGG CCCAGGAGGC CCTGCCTGAG
CCATACCTGT TCCTGTCCCC CCACGGGACT CCGGTAAGG AGGAGGACGG GGGAGGATAG GTGGACAAA GAGGTGACCC GGTCTCTCCG GGACGGGACTC

701 AAGCTTCCC AGCAGATCCA TGCTTCTCC TCCACCACCC TGGATGACAT CCTGCATGCG TTCTCTGAAG TCAGTGCTGC CCGTGTGGTG GGAGGCTATC
TTGCGAAGGG TCGTCTAGGT ACGAAAGAG AGGTGGTGG ACCTACTGTA GGACGTACCG AAGAGACTTC AGTCACGACG GCACACACAC CCTCCGATAG

801 TGCTCATGGT GGTCTTTGCA CCTGGCACCT TGCCCCCACC CCACCTCCAA CCAGTGCCCA CCTTGGGGG CCCCTGAGAC TGCCCTTTCC CCCCACAGCT
ACGAGTACCA CCCAGAACGT GGACCGTGGA ACGGGGTGG GGTGAGGTT GGTACAGGGT GGGACCCCTC GGGGACTCTG ACGGGAAGG GGGGTGTGGA

FIG. 10A

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901 GGCCTATGCC TGTGTGACCA TGCTGCGGTG GGA CTGCGCC CAGTCCCAGG GTTCCGTGGG CCTTGCCGGG G TACTGCTGG TGGCCCTGGC GGTGGCCTCA
CCGGATACGG ACACACTGGT ACGACGCCAC CCTGACGCGG GTCAGGGTCC CAAGGCACCC GGAACGGCCC CATGACGACC ACCGGGACCG CCACCGGAGT

1001 GGCCTTGGC TCTGTGCCCT GCTGGGCATC ACCTTCAATG CTGCCACTAC CCAGGTACGC CAGGACTGCA GGGCAGACTC AGTGCCAGTC ACCAGGCTTC
CCGGAACCCG AGACACGGGA CGAGCCGTAG TGGAA GTTAC GACGGTGATG GGTCCATGCG GTCCCTGACGT CCCGTCTGAG TCACGGTCTAG TGGTCCGAAG

1101 ACGGGTCTC AGCTGCCCGC TCCTCTGCC CTCCAGGTGC TGCCCTTCTT GACTCTGGA ATCGGCGTGG ATGACGTATT CCTGCTGGCG CATGCCCTTCA
TGCCAGGAG TCGACGGGCG AGGAGACGGG GAGGTCCACG ACGGGAAGAA CTGAGACCCT TAGCCGCACC TACTGCATAA GGACGACCGC GTACGGGAAGT

1201 CAGAGGCTCT GCCTGGCACC CCTCTCCAGG TGGGGCCTTG TCCCCCAGG CTCATCTGAG GCAGCTCAGC TTACTGGTTA AGAGCCTCTT GGTTC AAGTG
GTCTCCGAGA CGGACCGTGG GGAGAGGTCC ACCCCGGAAC AGGGGTCCC GAGTAGACTC CGTCGAGTCG AATGACCAAT TCTCGGAGAA CCAAGTTTAC

1301 ACCTTGGCT GCTAATGAAC CTCGGTGCCT CTGTGCCCA TGTGTAACA GGGGAATAA TAGTGCTGTG TCCTAAGGGT TATTGTTTGG ATCAGTGAAG
TGGAACCCGA CGATTACTTG GAGCCACGGA GAACAGGGGT ACACATTTGT CCCCCTTATT ATCAGCACAC AGGATTCCCA ATAACA AACC TAGTCACTTC

1401 TAACTCAAGT TGAATGCTTA GAACAGCCCA TCATACGTAC ATGTACCCA ATAAATGCTA GCCACTGTGT TATGACTGCC CCACCTCTGC ACCCCAAGTT
ATTGAGTTCA ACTTACGAAT CTGTGCGGT AGTATGCATG TACCATGGGT TATTTACGAT CCGTGACACA ATACTGACCG GGTGGAGACG TGGGGTTCAA

1501 CCTGAGCCTC CCCTTCACTC CACTTTGACA CGGCCCTTCC CTTGTGACCT GAGGGCAGGT CCCCCTCTG TCCTGGCAGG AGCGCATGGG CGAGTGTCTG
GGACTCGGAG GGGAAGTGAG GTGAAACTGT GCCGGGAGG GAACACTGGA CTCCCGTCCA GGGGTGAGAC AGGACCGTCC TCGCGTACCC GCTCACAGAC

1601 CAGCGCACGG GCACCAAGTGT TGTACTACA TCCATCAACA ACATGGCCGC CTTCTCATG GTCGCCCTCG TTCCCATCCC TGGCGTGCGA GCCTTCTCCC
GTGCGGTGCC CGTGGTCACA ACATGAGTGT AGGTAGTTGT TGTACCGGCG GAAGGAGTAC CGACGGGAGC AAGGGTAGGG ACGCGACGCT CGGAAGAGGG

1701 TACAGCCTGG ACCTACGGCG GCGCCACTGC CAGCGCCTTG ATGTGCTCTG CTGCTTCTCC AGGTACTGCC TGGCCCCCAG CCCCTTCTC CCGTGACCCA
ATGTCGGACC TGGATGCCCG CGCGGTGACG GTCGCGGAAC TACACGAGAC GACGAAGAGG TCCATGACGG ACGCGGGTC GGGGAAGGAG GGCAC TGGGT

1801 CGCCAGCCTG TCCCCTCACC AGCATTTCAA GGCACAGACC TGTATCCAC TCTTACCTC TTCCAGTCCC TGCTCTGCTC AGGTGATTCA GATCCTGCC
GCGGTCCGAC AGGGAGTGG TCGTAAAGTT CCGTGTCTGG ACAGTAGGTG AGAGATGGAG AAGGTCAGGG ACGAGACGAG TCCACTAAGT CTAGGACGGG

1901 CAGGAGCTGG GGGACGGGAC AGTACCAGTG GGCATTGCCC ACCTCACTGC CACAGTTCAA GCCTTTACCC ACTGTGAAGC CAGCAGCCAG CATGTGGTCA
GTCCTCGACC CCCTGCCCTG TCATGCTCAC CCGTAAACGG TGGAGTGACG GTGTCAAGTT CGGAAATGGG TGACACTTCG GTCGTCTGTC GTACACCAAGT

2001 CCATCCTGCC TCCCCAAGCC CACCTGGTGC CCCCACCTC TGACCCACTG GGCTCTGAGC TCTTCAGCCC TGGAGGGTCC ACACGGGACC TTCTAGGCCA
GGTAGGACCG AGGGTTCCG GTGGACCACG GGGGTGGAAG ACTGGGTGAC CCGAGACTCG AGAAGTCGGG ACCTCCCAGG TGTGCCCTGG AAGATCCGGT

FIG. 10B

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2101 GGAGGAGGAG ACAAGGCAGA AGGCAGCCTG CAAGTCCCTG CCCTGTGCC GCTGGAATCT TGCCCATTTT GCGCGCTATC AGTTTGCCCC GTTGCTGCTC
CCTCCTCCTC TGTTCCGTCT TCCGTGGAC GTTCAGGGAC GGGACACGG CGACCTTAGA ACGGGTAAAG CCGCGGATAG TCAAAACGGG CAACGACGAG

2201 CAGTCACATG CCAAGGCCAT CGTGCTGGTG CTCTTTGGTG CCTGAGCCTC TACGGAGCCA CCTTGGTGCA AGACGGCCTG GCCCTGACGG
GTCAGTGTAC GGTTCGGTA GCACGACCAC GAGAAACCAC GAGACTCGAG ATGCCTCGGT GGAACACAGT TCTGCCGGAC CGGACTGCC

2301 ATGTGGTGCC TCGGGGCACC AAGGAGCATG CCTTCCTGAG CGCCAGCTC AGGTACTTCT CCCTGTACGA GGTGGCCCTG GTGACCCAGG GTGGCTTTGA
TACACCACGG AGCCCCGTGG TTCTCTGTAC GGAAGGACTC GCGGTCTGAG TCCATGAAGA GGGACATGCT CCACCGGGAC CACTGGGTCC CACCGAAACT

2401 CTACGCCAC TCCAAAGCG CCCTCTTTGA TCTGCACCAG CGCTTCAGTT CCCTCAAGGC GGTGCTGCCC CCACCGGCCA CCCAGGCACC CCGCACCTGG
GATCGGGTG AGGGTTGCG GGGAGAACT AGACGTGGTC GCGAAGTCAA GGGAGTTCCG CCACGACGGG GGTGGCCGGT GGTCCGTGG GCGTGGACC

2501 CTGCACTATT ACCGCAACTG GCTACAGGGA ATCCAGGCTG CCTTTGACCA GGACTGGGT TCTGGGCGCA TCACCCGCCA CTCGTACCGC AATGGCTCTG
GACGTGATAA TGGCGTTGAC CGATGTCCCT TAGGTCCGAC GGAAACTGGT CCTGACCCGA AGACCCGGT AGTGGCGGT GAGCATGGCG TTACCGAGAC

2601 AGGATGGGC CCTGGCCTAC AAGCTGCTCA TCCAGACTGG AGACGCCAG GAGCCTCTGG ATTTCAGCCA GGTGGGAGA GGGCTGGAGG GTTCCACTAG
TCCTACCCCG GGACCGGATG TTCGACGAGT AGGTCTGACC TCTGGGGTC CTCGGAGACC TAAAGTCGGT CCAACCTCTT CCCGACCTCC CCAGGTGATC

2701 TACAGGGGCT GCAGGCCCTCC TGGGCCCAGG CCTTCAGCCC TCTCTGCC TCAGCTGAC CACAAGGAAG CTGGTGGACA GAGAGGACT GATTCCACCC
ATGTCCCGA CGTCCGGAG ACCCGGTCC GGAAGTCGG AGAGAGGGAG ACGTCGACTG GTGTTCTTC GACCACCTGT CTCTCCCTGA CTAAGGTGGG

2801 GAGCTCTTCT ACATGGGGCT GACCGTGTG GTGAGCAGTG ACCCCCTGG TCTGGCAGCC TCACAGGCCA ACTTCTACCC CCCACCTCTT GAATGGCTGC
CTCGAGAAGA TGTACCCCGA CTGGCACACC CACTCGTCAC TGGGGGACCC AGACCGTCGG AGTGTCCGT TGAAGATGGG GGTGGAGGA CTTACCGAGC

2901 ACGACAAATA CGACACCACG GGGGAGAACC TTCGCAGTGA GTCTTGGGG GAGCTCGGCA AGAGCCTCAG CCTCGCCAC ACAAGCCCTG AGCCTGAGGC
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3001 CCTGCCCACT CTGCCCCGTG CTCACCGCCC TGTCCTCTC CCTCTTCTCC CTTCCTCTCC CCGCCAGCT CAGCCCTTGG AGTTTGCCCA
GGACGGGTGA GACGGGSCAC GAGTGGCGG ACAGGGAGAG GGAGAGAGG GAAGGGGAGG GGAGGTGTCA GGGCGGTCA GTCCGGAACC TCAACCGGGT

FIG. 10C

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3101 GTTCCCTTC CTGCTGCTG GCCTCCAGAA GACTGCAGAC TTTGTGGAGG CCATCGAGGG GGCCCGGGCA GCATGGCAG AGGCCGGCCA GGCTGGGGTG
CAAGGGGAAG GACGACGCAC CGGAGGTCTT GTGACGTCTG AAACACCTCC GGTAGCTCCC CCGGCCCGT CGTACCGGTC TCCGGCCGGT CCGACCCAC
3201 CACGCCCTACC CCAGCGGCTC CCCCTTCCTC TTCTGGGAAC AGTATCTGGG CCTGCGGCGC TGCTTCCTGC TGGCCGTCTG CATCTGCTG GTGTGCACCT
GTGCGGATGG GGTGCGCGAG GGGGAAGGAG AAGACCCTTG TCATAGACCC GGACGCGCGG ACGAAGGACG ACCGGCAGAC GTAGGACGAC CACACGTGAA
3301 TCCTCGTCTG TGCTCTGCTG CTCCTCAACC CCTGGACGGC TGGCCTCATA GTGAGTGCTT GCAGAGTGG GGACAGAGAC ACCCCACCCT TCCCTGCCCCA
AGGAGCAGAC ACGAGACGAC GAGGAGTTGG GGACCTGCCG ACCGGAGTAT CACTCACGAA CGTCCTCACC CCTGTCTCTG TGGGGTGGGA AGGGACGGGT
3401 GCCTGTCTC CCTCCTGCCA GGAGCCCTCT GTGAGCCCTG TCTCCCTCAG GTGCTGGTCC TGGCGATGAT GACAGTGGAA CTCCTTTGGTA TCATGGGTTT
CGGACAGTAG GGAGGACGGT CCTCGGGAGA CACTCGGGAC AGAGGGAGTC CACGACCAGG ACCGCTACTA CTGTCACCTT GAGAAACCAT AGTACCCAAA
3501 CCTGGGCATC AAGCTGAGTG CCATCCCCCT GGTGATCCTT GTGGCCTCTG TAGGCATTGG CGTTGAGTTC ACAGTCCACG TGGCTCTGGT GAGCACGGGC
GGACCCGTAG TTCGACTCAC GGTAGGGGCA CCACTAGGAA CACCGGAGAC ATCCGTAAAC GCAACTCAAG TGTCAGGTGC ACCGAGACCA CTCGTGCCCCG
3601 ACCCCGGGA GGGACCAATC AGCTGATTCA GTATTCAACA CATATTGTTT AAGCCCTAC TATGTGCTAG GTACTATTTA AGAATTTGGG CTGGGTGGAC
TGGGGCCCT CCCTGGTTAG TCGACTAAGT CATAAGTTGT GTATAACAAG TTCGGGGATG ATACACGATC CATGATAAAT TCTTAAACCC GACCCACCTG
3701 GTGGTGGCTC ATTCTGTAA TCCAGCACT TTGGGAGGCC GAGGCGGGTG GATCACCTGA GGTGCGGAGT TCGAAACCAG CCTGGCCAAC ATGGTGAAC
CACCACCGAG TAAGGACATT AGGGTCGTGA AACCTCCCG CTCCGCCAC CTAGTGAGT CCAGCCCTCA AGCTTTGGTC GGACCGGTTG TACCACCTTG
3801 CCTGTCTTTA CTAAAAATAC AAAAAATTAG CCAGCGGTGG TGGCACATGC CAGTACTTTG GAGGCTGAGG CAGAATTGCT TGAACCTGGG
GGACAGAAAT GATTTTATG TTTTATATG GGTCCGCACC ACCGTGTACG GTCATCAGGG TCGATGAAAC CTCCGACTCC GTCTTAACGA ACTTGGACCC
3901 AGGCGAAGT TGCAGTGAGC TGAGATCGTG CCATTGCACT CCAGCCTGGG CAACAAGAGT GCAACTCTCC GTCTCAAAA AAAAAAAA AAGGGCGGC
TCCGCTTCCA ACGTCACTCG ACTCACTCG GGTAAACGTGA GGTCGGACCC GTTGTCTCA CGTTGAGAGG CAGAGTTTTT TTTTTTTTTT TTCCCGCCCG

4001 GCGA
CGCT

FIG. 10D

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Clone 16.1 human patched 2
> 1 ngth: 2082 bp

> (SEQ ID NO:9)

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101 GCTCCACTCT GGCTTCGTGC TTACTTCCAG GGCCTGCTCT TCTCTCTGGG ATGGGGGATC CAGAGACATT GTGGCAAAAGT GCTCTTTCTG GGACTGTTGG
   CGAGGTGAGA CCGAAGCAGC AATGAAGGTC CCGGACGAGA AGAGAGACCC TAGCCCTAG GTCTCTGTAA CACCGTTTCA CGAGAAAGAC CCTGACAACC

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   GAACCGGAGG TGGAGGTCCG TCGGGAGTGA CCGTCATTTC AGGTTTCATAG TGAGATACCC TTCAGGACCC TAAACTTGT TTAGACGATG TTCAGTCTCTC

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701 GAGGGCTTCC GGGAGCTGCT AGACAAGGCA CAGGTGGGCC AGGCCTACGT GGGGCGGCC TGTCTGCACC CTGATGACCT CCACTGCCCA CCTAGTGCCC
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901 GCTGGGAGGC ATGGCCAGAG ACCCCCAAGG AGAGTGCTG AGGGCAGAG CCCTGTCAG CACCTTCTTG CTGATGAGTC CCGCCAGCT GTACGAGCAT
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```

FIG. 11A

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1001 TTCCGGGGTG ACTATCAGAC ACATGACATT GGCTGGAGTG AGGAGCAGGC CAGCACAGTG CTACAAGCCT GGCAGGGCGG CTTTGTGCAG CTGGCCCCAGG
AAGGCCCCAC TGATAGTCTG TGTAAGTCTG CCGACCTCAC TCCTCGTCCG GTCGTGTAC GATGTTCCGA CCGTCGCCGC GAAACACGTC GACCCGGGTCC

1101 AGGCCCTGCC TGAGAACGCT TCCAGCAGA TCCATGCCCTT CTCCTCCACC ACCCTGGATA ACATCCTGCA TGCCTTCTCT GAAGTCAGTG CTGCCCGTGT
TCCGGGACGG ACTCTTGCGA AGGTCGTCT AGGTACGGAA GAGGAGGTGG TGGACCTAT TGTAGGACGT ACGCAAGAGA CTTCACTCAG GACGGGCACA

1201 GGTGGGAGGC TATCTGCTCA TGCTGGCCTA TCCCTGTGTG ACCATGCTGC GGTGGACTG CGCCAGTCC CAGGTTCCG TGGGCTTGC CGGGGTACTG
CCACCCTCCG ATAGACGAGT ACGACCGGAT ACGACACAC TGGTACGACG CCACCCTGAC GCGGGTCAGG GTCCCAAGGC ACCCGGAACG GCCCCATGAC

1301 CTGGTGGCCC TGGCGGTGGC CTCAGGCCTT GGGCTCTGTG CCCTGCTCGG CATCACCTTC AATGCTGCCA CTACCCAGGT GCTGCCCTTC TTGGCTCTGG
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1701 GGAGCTGGG GACGGACAG TACCAGTGG CATGCCAC CTCACTGCCA CAGTTCAAGC CTTTACCCAC TGTGAAGCCA GCAGCCAGCA TGTGTCACC
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1901 AGGAGGAGAC AAGGAGAAG GCAGCCTGCA AGTCCCTGCC CTGTGCCCGC TGGAACTTG CCCATTTCGC CCCGGAATTC CTGCAGCCCC GGGGATCCAC
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ATCAAGATCT CGCCGGGGT GCGGCCACCT CGAGGTCGAA AACAAAGGAA ATCACTCCA ATTAACGCG GAACCCATAG AA

FIG. 11B

Sequence Listing

<110> Genentech, Inc.

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	Ala Lys Leu Gln Gly Gly Ser Ala Tyr Leu Pro Gly Arg Pro Asp	200	205	210
5	Ile Gln Trp Thr Asn Leu Asp Pro Glu Gln Leu Leu Glu Glu Leu	215	220	225
	Gly Pro Phe Ala Ser Leu Glu Gly Phe Arg Glu Leu Leu Asp Lys	230	235	240
10	Ala Gln Val Gly Gln Ala Tyr Val Gly Arg Pro Cys Leu His Pro	245	250	255
	Asp Asp Leu His Cys Pro Pro Ser Ala Pro Asn His His Ser Arg	260	265	270
	Gln Ala Pro Asn Val Ala His Glu Leu Ser Gly Gly Cys His Gly	275	280	285
15	Phe Ser His Lys Phe Met His Trp Gln Glu Glu Leu Leu Leu Gly	290	295	300
	Gly Met Ala Arg Asp Pro Gln Gly Glu Leu Leu Arg Ala Glu Ala	305	310	315
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	His Phe Arg Gly Asp Tyr Gln Thr His Asp Ile Gly Trp Ser Glu	335	340	345
	Glu Gln Ala Ser Thr Val Leu Gln Ala Trp Gln Arg Arg Phe Val	350	355	360
25	Gln Leu Ala Gln Glu Ala Leu Pro Glu Asn Ala Ser Gln Gln Ile	365	370	375
	His Ala Phe Ser Ser Thr Thr Leu Asp Asp Ile Leu His Ala Phe	380	385	390
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	Leu Ala Tyr Ala Cys Val Thr Met Leu Arg Trp Asp Cys Ala Gln	410	415	420
	Ser Gln Gly Ser Val Gly Leu Ala Gly Val Leu Leu Val Ala Leu	425	430	435
35	Ala Val Ala Ser Gly Leu Gly Leu Cys Ala Leu Leu Gly Ile Thr	440	445	450
	Phe Asn Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly	455	460	465

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	Ala Ala Phe Leu Met Ala Ala Leu Val Pro Ile Pro Ala Leu Arg	515	520	525
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	Asp Gly Thr Val Pro Val Gly Ile Ala His Leu Thr Ala Thr Val	590	595	600
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	Ile Leu Pro Pro Gln Ala His Leu Val Pro Pro Pro Ser Asp Pro	620	625	630
	Leu Gly Ser Glu Leu Phe Ser Pro Gly Gly Ser Thr Arg Asp Leu	635	640	645
25	Leu Gly Gln Glu Glu Glu Thr Arg Gln Lys Ala Ala Cys Lys Ser	650	655	660
	Leu Pro Cys Ala Arg Trp Asn Leu Ala His Phe Ala Arg Tyr Gln	665	670	675
30	Phe Ala Pro Leu Leu Leu Gln Ser His Ala Lys Ala Ile Val Leu	680	685	690
	Val Leu Phe Gly Ala Leu Leu Gly Leu Ser Leu Tyr Gly Ala Thr	695	700	705
	Leu Val Gln Asp Gly Leu Ala Leu Thr Asp Val Val Pro Arg Gly	710	715	720
35	Thr Lys Glu His Ala Phe Leu Ser Ala Gln Leu Arg Tyr Phe Ser	725	730	735
	Leu Tyr Glu Val Ala Leu Val Thr Gln Gly Gly Phe Asp Tyr Ala	740	745	750

	His Ser Gln Arg Ala Leu Phe Asp Leu His Gln Arg Phe Ser Ser	755	760	765
	Leu Lys Ala Val Leu Pro Pro Pro Ala Thr Gln Ala Pro Arg Thr	770	775	780
5	Trp Leu His Tyr Tyr Arg Asn Trp Leu Gln Gly Ile Gln Ala Ala	785	790	795
	Phe Asp Gln Asp Trp Ala Ser Gly Arg Ile Thr Arg His Ser Tyr	800	805	810
10	Arg Asn Gly Ser Glu Asp Gly Ala Leu Ala Tyr Lys Leu Leu Ile	815	820	825
	Gln Thr Gly Asp Ala Gln Glu Pro Leu Asp Phe Ser Gln Leu Thr	830	835	840
	Thr Arg Lys Leu Val Asp Arg Glu Gly Leu Ile Pro Pro Glu Leu	845	850	855
15	Phe Tyr Met Gly Leu Thr Val Trp Val Ser Ser Asp Pro Leu Gly	860	865	870
	Leu Ala Ala Ser Gln Ala Asn Phe Tyr Pro Pro Pro Pro Glu Trp	875	880	885
20	Leu His Asp Lys Tyr Asp Thr Thr Gly Glu Asn Leu Arg Ile Pro	890	895	900
	Pro Ala Gln Pro Leu Glu Phe Ala Gln Phe Pro Phe Leu Leu Arg	905	910	915
	Gly Leu Gln Lys Thr Ala Asp Phe Val Glu Ala Ile Glu Gly Ala	920	925	930
25	Arg Ala Ala Cys Ala Glu Ala Gly Gln Ala Gly Val His Ala Tyr	935	940	945
	Pro Ser Gly Ser Pro Phe Leu Phe Trp Glu Gln Tyr Leu Gly Leu	950	955	960
30	Arg Arg Cys Phe Leu Leu Ala Val Cys Ile Leu Leu Val Cys Thr	965	970	975
	Phe Leu Val Cys Ala Leu Leu Leu Leu Asn Pro Trp Thr Ala Gly	980	985	990
	Leu Ile Val Leu Val Leu Ala Met Met Thr Val Glu Leu Phe Gly	995	1000	1005
35	Ile Met Gly Phe Leu Gly Ile Lys Leu Ser Ala Ile Pro Val Val	1010	1015	1020
	Ile Leu Val Ala Ser Val Gly Ile Gly Val Glu Phe Thr Val His	1025	1030	1035

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5 Ala Ile Ser Thr Leu Leu Gly Leu Leu Met Leu Ala Gly Ser His
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10 Thr Leu Leu Gly Leu Leu His Gly Leu Val Leu Leu Pro Val Leu
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Leu Ser Ile Leu Gly Pro Pro Pro Glu Val Ile Gln Met Tyr Lys
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Glu Ser Pro Glu Ile Leu Ser Pro Pro Ala Pro Gln Gly Gly Gly
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15 Leu Arg Trp Gly Ala Ser Ser Ser Leu Pro Gln Ser Phe Ala Arg
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Val Thr Thr Ser Met Thr Val Ala Ile His Pro Pro Pro Leu Pro
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20 Gly Ala Tyr Ile His Pro Ala Pro Asp Glu Pro Pro Trp Ser Pro
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Ala Ala Thr Ser Ser Gly Asn Leu Ser Ser Arg Gly Pro Gly Pro
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10 Val Val Leu Ala Cys Thr Phe Leu Val Cys Ala Val Phe Leu Leu
 35 40 45

Asn Pro Trp Thr Ala Gly Ile Ile Val Met Val Leu Ala Leu Met
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	Leu	Gly	Leu	Val	Ala	Phe	Gly	Ala	Leu	Ala	Leu	Gly	Leu	Arg	Val	
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15	Ala	Val	Ile	Glu	Thr	Asp	Leu	Glu	Gln	Leu	Trp	Val	Glu	Val	Gly	
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	Ser	Arg	Val	Ser	Gln	Glu	Leu	His	Tyr	Thr	Lys	Glu	Lys	Leu	Gly	
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	Ile	Gln	Trp	Thr	Asn	Leu	Asp	Pro	Gln	Gln	Leu	Leu	Glu	Glu	Leu	
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		Gly Thr Ala Arg Asp Leu Gln Gly Gln Leu Leu Arg Ala Glu Ala				
		305		310		315
		Leu Gln Ser Thr Phe Leu Leu Met Ser Pro Arg Gln Leu Tyr Glu				
		320		325		330
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		335		340		345
		Glu Gln Ala Ser Met Val Leu Gln Ala Trp Gln Arg Arg Phe Val				
		350		355		360
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		365		370		375
		His Ala Phe Ser Ser Thr Thr Leu Asp Asp Ile Leu Arg Ala Phe				
		380		385		390
		Ser Glu Val Ser Thr Thr Arg Val Val Gly Gly Tyr Leu Leu Met				
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		410		415		420
		Ser Gln Gly Ala Val Gly Leu Ala Gly Val Leu Leu Val Ala Leu				
		425		430		435
25		Ala Val Ala Ser Gly Leu Gly Leu Cys Ala Leu Leu Gly Ile Thr				
		440		445		450
		Phe Asn Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly				
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		500		505		510
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	Arg Arg His Arg Gln Arg Leu Asp Val Leu Cys Cys Phe Ser Ser	560	565	570
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	Asp Arg Ala Val Pro Val Gly Ile Ala His Leu Thr Ala Thr Val	590	595	600
10	Gln Ala Phe Thr His Cys Glu Ala Ser Ser Gln His Val Val Thr	605	610	615
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	Leu Gly Ser Glu Leu Tyr Ser Pro Gly Gly Ser Thr Arg Asp Leu	635	640	645
15	Leu Ser Gln Glu Glu Gly Thr Gly Pro Gln Ala Ala Cys Arg Pro	650	655	660
	Leu Leu Cys Ala His Trp Thr Leu Ala His Phe Ala Arg Tyr Gln	665	670	675
20	Phe Ala Pro Leu Leu Leu Gln Thr Arg Ala Lys Ala Leu Val Leu	680	685	690
	Leu Phe Phe Gly Ala Leu Leu Gly Leu Ser Leu Tyr Gly Ala Thr	695	700	705
	Leu Val Gln Asp Gly Leu Ala Leu Thr Asp Val Val Pro Arg Gly	710	715	720
25	Thr Lys Glu His Ala Phe Leu Ser Ala Gln Leu Arg Tyr Phe Ser	725	730	735
	Leu Tyr Glu Val Ala Leu Val Thr Gln Gly Gly Phe Asp Tyr Ala	740	745	750
30	His Ser Gln Arg Ala Leu Phe Asp Leu His Gln Arg Phe Ser Ser	755	760	765
	Leu Lys Ala Val Leu Pro Pro Pro Ala Thr Gln Ala Pro Arg Thr	770	775	780
	Trp Leu His Tyr Tyr Arg Ser Trp Leu Gln Gly Ile Gln Ala Ala	785	790	795
35	Phe Asp Gln Asp Trp Ala Ser Gly Arg Ile Thr Cys His Ser Tyr	800	805	810
	Arg Asn Gly Ser Glu Asp Gly Ala Leu Ala Tyr Lys Leu Leu Ile	815	820	825

	Gln Thr Gly Asn Ala Gln Glu Pro Leu Asp Phe Ser Gln Leu Thr	830	835	840
	Thr Arg Lys Leu Val Asp Lys Glu Gly Leu Ile Pro Pro Glu Leu	845	850	855
5	Phe Tyr Met Gly Leu Thr Val Trp Val Ser Ser Asp Pro Leu Gly	860	865	870
	Leu Ala Ala Ser Gln Ala Asn Phe Tyr Pro Pro Pro Pro Glu Trp	875	880	885
10	Leu His Asp Lys Tyr Asp Thr Thr Gly Glu Asn Leu Arg Ile Pro	890	895	900
	Ala Ala Gln Pro Leu Glu Phe Ala Gln Phe Pro Phe Leu Leu His	905	910	915
	Gly Leu Gln Lys Thr Ala Asp Phe Val Glu Ala Ile Glu Gly Ala	920	925	930
15	Arg Ala Ala Cys Thr Glu Ala Gly Gln Ala Gly Val His Ala Tyr	935	940	945
	Pro Ser Gly Ser Pro Phe Leu Phe Trp Glu Gln Tyr Leu Gly Leu	950	955	960
20	Arg Arg Cys Phe Leu Leu Ala Val Cys Ile Leu Leu Val Cys Thr	965	970	975
	Phe Leu Val Cys Ala Leu Leu Leu Leu Ser Pro Trp Thr Ala Gly	980	985	990
	Leu Ile Val Leu Val Leu Ala Met Met Thr Val Glu Leu Phe Gly	995	1000	1005
25	Ile Met Gly Phe Leu Gly Ile Lys Leu Ser Ala Ile Pro Val Val	1010	1015	1020
	Ile Leu Val Ala Ser Ile Gly Ile Gly Val Glu Phe Thr Val His	1025	1030	1035
30	Val Ala Leu Gly Phe Leu Thr Ser His Gly Ser Arg Asn Leu Arg	1040	1045	1050
	Ala Ala Ser Ala Leu Glu Gln Thr Phe Ala Pro Val Thr Asp Gly	1055	1060	1065
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					20					25					30	
	Ala	Leu	Lys	Phe	Ile	Pro	Lys	Leu	Gly	Arg	Ser	Glu	Lys	Glu	Leu	
					35					40					45	
5	Arg	Asn	Leu	Gln	Arg	Glu	Ile	Glu	Ile	Met	Arg	Gly	Leu	Arg	His	
					50					55					60	
	Pro	Asn	Ile	Val	His	Met	Leu	Asp	Ser	Phe	Glu	Thr	Asp	Lys	Glu	
					65					70					75	
10	Val	Val	Val	Val	Thr	Asp	Tyr	Ala	Glu	Gly	Glu	Leu	Phe	Gln	Ile	
					80					85					90	
	Leu	Glu	Asp	Asp	Gly	Lys	Leu	Pro	Glu	Asp	Gln	Val	Gln	Ala	Ile	
					95					100					105	
	Ala	Ala	Gln	Leu	Val	Ser	Ala	Leu	Tyr	Tyr	Leu	His	Ser	His	Arg	
					110					115					120	
15	Ile	Leu	His	Arg	Asp	Met	Lys	Pro	Gln	Asn	Ile	Leu	Leu	Ala	Lys	
					125					130					135	
	Gly	Gly	Gly	Ile	Lys	Leu	Cys	Asp	Phe	Gly	Phe	Ala	Arg	Ala	Met	
					140					145					150	
20	Ser	Thr	Asn	Thr	Met	Val	Leu	Thr	Ser	Ile	Lys	Gly	Thr	Pro	Leu	
					155					160					165	
	Tyr	Met	Ser	Pro	Glu	Leu	Val	Glu	Glu	Arg	Pro	Tyr	Asp	His	Thr	
					170					175					180	
	Ala	Asp	Leu	Trp	Ser	Val	Gly	Cys	Ile	Leu	Tyr	Glu	Leu	Ala	Val	
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25	Gly	Thr	Pro	Pro	Phe	Tyr	Ala	Thr	Ser	Ile	Phe	Gln	Leu	Val	Ser	
					200					205					210	
	Leu	Ile	Leu	Lys	Asp	Pro	Val	Arg	Trp	Pro	Ser	Thr	Ile	Ser	Pro	
					215					220					225	
30	Cys	Phe	Lys	Asn	Phe	Leu	Gln	Gly	Leu	Leu	Thr	Lys	Asp	Pro	Arg	
					230					235					240	
	Gln	Arg	Leu	Ser	Trp	Pro	Asp	Leu	Leu	Tyr	His	Pro	Phe	Ile	Ala	
					245					250					255	
	Gly	His	Val	Thr	Ile	Ile	Thr	Glu	Pro	Ala	Gly	Pro	Asp	Leu	Gly	
					260					265					270	
35	Thr	Pro	Phe	Thr	Ser	Arg	Leu	Pro	Pro	Glu	Leu	Gln	Val	Leu	Lys	
					275					280					285	
	Asp	Glu	Gln	Ala	His	Arg	Leu	Ala	Pro	Lys	Gly	Asn	Gln	Ser	Arg	
					290					295					300	

	Ile	Leu	Thr	Gln	Ala	Tyr	Lys	Arg	Met	Ala	Glu	Glu	Ala	Met	Gln	
					305					310					315	
	Lys	Lys	His	Gln	Asn	Thr	Gly	Pro	Ala	Leu	Glu	Gln	Glu	Asp	Lys	
					320					325					330	
5	Thr	Ser	Lys	Val	Ala	Pro	Gly	Thr	Ala	Pro	Leu	Pro	Arg	Leu	Gly	
					335					340					345	
	Ala	Thr	Pro	Gln	Glu	Ser	Ser	Leu	Leu	Ala	Gly	Ile	Leu	Ala	Ser	
					350					355					360	
10	Glu	Leu	Lys	Ser	Ser	Trp	Ala	Lys	Ser	Gly	Thr	Gly	Glu	Val	Pro	
					365					370					375	
	Ser	Ala	Pro	Arg	Glu	Asn	Arg	Thr	Thr	Pro	Asp	Cys	Glu	Arg	Ala	
					380					385					390	
	Phe	Pro	Glu	Glu	Arg	Pro	Glu	Val	Leu	Gly	Gln	Arg	Ser	Thr	Asp	
					395					400					405	
15	Val	Val	Asp	Leu	Glu	Asn	Glu	Glu	Pro	Asp	Ser	Asp	Asn	Glu	Trp	
					410					415					420	
	Gln	His	Leu	Leu	Glu	Thr	Thr	Glu	Pro	Val	Pro	Ile	Gln	Leu	Lys	
					425					430					435	
20	Ala	Pro	Leu	Thr	Leu	Leu	Cys	Asn	Pro	Asp	Phe	Cys	Gln	Arg	Ile	
					440					445					450	
	Gln	Ser	Gln	Leu	His	Glu	Ala	Gly	Gly	Gln	Ile	Leu	Lys	Gly	Ile	
					455					460					465	
	Leu	Glu	Gly	Ala	Ser	His	Ile	Leu	Pro	Ala	Phe	Arg	Val	Leu	Ser	
					470					475					480	
25	Ser	Leu	Leu	Ser	Ser	Cys	Ser	Asp	Ser	Val	Ala	Leu	Tyr	Ser	Phe	
					485					490					495	
	Cys	Arg	Glu	Ala	Gly	Leu	Pro	Gly	Leu	Leu	Leu	Ser	Leu	Leu	Arg	
					500					505					510	
30	His	Ser	Gln	Glu	Ser	Asn	Ser	Leu	Gln	Gln	Gln	Ser	Trp	Tyr	Gly	
					515					520					525	
	Thr	Phe	Leu	Gln	Asp	Leu	Met	Ala	Val	Ile	Gln	Ala	Tyr	Phe	Ala	
					530					535					540	
	Cys	Thr	Phe	Asn	Leu	Glu	Arg	Ser	Gln	Thr	Ser	Asp	Ser	Leu	Gln	
					545					550					555	
35	Val	Phe	Gln	Glu	Ala	Ala	Asn	Leu	Phe	Leu	Asp	Leu	Leu	Gly	Lys	
					560					565					570	
	Leu	Leu	Ala	Gln	Pro	Asp	Asp	Ser	Glu	Gln	Thr	Leu	Arg	Arg	Asp	
					575					580					585	

	Ser	Leu	Met	Cys	Phe	Thr	Val	Leu	Cys	Glu	Ala	Met	Asp	Gly	Asn	590	595	600
	Ser	Arg	Ala	Ile	Ser	Lys	Ala	Phe	Tyr	Ser	Ser	Leu	Leu	Thr	Thr	605	610	615
5	Gln	Gln	Val	Val	Leu	Asp	Gly	Leu	Leu	His	Gly	Leu	Thr	Val	Pro	620	625	630
	Gln	Leu	Pro	Val	His	Thr	Pro	Gln	Gly	Ala	Pro	Gln	Val	Ser	Gln	635	640	645
10	Pro	Leu	Arg	Glu	Gln	Ser	Glu	Asp	Ile	Pro	Gly	Ala	Ile	Ser	Ser	650	655	660
	Ala	Leu	Ala	Ala	Ile	Cys	Thr	Ala	Pro	Val	Gly	Leu	Pro	Asp	Cys	665	670	675
	Trp	Asp	Ala	Lys	Glu	Gln	Val	Cys	Trp	His	Leu	Ala	Asn	Gln	Leu	680	685	690
15	Thr	Glu	Asp	Ser	Ser	Gln	Leu	Arg	Pro	Ser	Leu	Ile	Ser	Gly	Leu	695	700	705
	Gln	His	Pro	Ile	Leu	Cys	Leu	His	Leu	Leu	Lys	Val	Leu	Tyr	Ser	710	715	720
20	Cys	Cys	Leu	Val	Ser	Glu	Gly	Leu	Cys	Arg	Leu	Leu	Gly	Gln	Glu	725	730	735
	Pro	Leu	Ala	Leu	Glu	Ser	Leu	Phe	Met	Leu	Ile	Gln	Gly	Lys	Val	740	745	750
	Lys	Val	Val	Asp	Trp	Glu	Glu	Ser	Thr	Glu	Val	Thr	Leu	Tyr	Phe	755	760	765
25	Leu	Ser	Leu	Leu	Val	Phe	Arg	Leu	Gln	Asn	Leu	Pro	Cys	Gly	Met	770	775	780
	Glu	Lys	Leu	Gly	Ser	Asp	Val	Ala	Thr	Leu	Phe	Thr	His	Ser	His	785	790	795
30	Val	Val	Ser	Leu	Val	Ser	Ala	Ala	Ala	Cys	Leu	Leu	Gly	Gln	Leu	800	805	810
	Gly	Gln	Gln	Gly	Val	Thr	Phe	Asp	Leu	Gln	Pro	Met	Glu	Trp	Met	815	820	825
	Ala	Ala	Ala	Thr	His	Ala	Leu	Ser	Ala	Pro	Ala	Glu	Val	Arg	Leu	830	835	840
35	Thr	Pro	Pro	Gly	Ser	Cys	Gly	Phe	Tyr	Asp	Gly	Leu	Leu	Ile	Leu	845	850	855
	Leu	Leu	Gln	Leu	Leu	Thr	Glu	Gln	Gly	Lys	Ala	Ser	Leu	Ile	Arg	860	865	870

	Asp Met Ser Ser Ser Glu Met Trp Thr Val Leu Trp His Arg Phe	875	880	885
	Ser Met Val Leu Arg Leu Pro Glu Glu Ala Ser Ala Gln Glu Gly	890	895	900
5	Glu Leu Ser Leu Ser Ser Pro Pro Ser Pro Glu Pro Asp Trp Thr	905	910	915
	Leu Ile Ser Pro Gln Gly Met Ala Ala Leu Leu Ser Leu Ala Met	920	925	930
10	Ala Thr Phe Thr Gln Glu Pro Gln Leu Cys Leu Ser Cys Leu Ser	935	940	945
	Gln His Gly Ser Ile Leu Met Ser Ile Leu Lys His Leu Leu Cys	950	955	960
	Pro Ser Phe Leu Asn Gln Leu Arg Gln Ala Pro His Gly Ser Glu	965	970	975
15	Phe Leu Pro Val Val Val Leu Ser Val Cys Gln Leu Leu Cys Phe	980	985	990
	Pro Phe Ala Leu Asp Met Asp Ala Asp Leu Leu Ile Val Val Leu	995	1000	1005
20	Ala Asp Leu Arg Asp Ser Glu Val Ala Ala His Leu Leu Gln Val	1010	1015	1020
	Cys Cys Tyr His Leu Pro Leu Met Gln Val Glu Leu Pro Ile Ser	1025	1030	1035
	Leu Leu Thr Arg Leu Ala Leu Met Asp Pro Thr Ser Leu Asn Gln	1040	1045	1050
25	Phe Val Asn Thr Val Ser Ala Ser Pro Arg Thr Ile Val Ser Phe	1055	1060	1065
	Leu Ser Val Ala Leu Leu Ser Asp Gln Pro Leu Leu Thr Ser Asp	1070	1075	1080
30	Leu Leu Ser Leu Leu Ala His Thr Ala Arg Val Leu Ser Pro Ser	1085	1090	1095
	His Leu Ser Phe Ile Gln Glu Leu Leu Ala Gly Ser Asp Glu Ser	1100	1105	1110
	Tyr Arg Pro Leu Arg Ser Leu Leu Gly His Pro Glu Asn Ser Val	1115	1120	1125
35	Arg Ala His Thr Tyr Arg Leu Leu Gly His Leu Leu Gln His Ser	1130	1135	1140
	Met Ala Leu Arg Gly Ala Leu Gln Ser Gln Ser Gly Leu Leu Ser	1145	1150	1155

Leu Leu Leu Leu Gly Leu Gly Asp Lys Asp Pro Val Val Arg Cys
 1160 1165 1170
 Ser Ala Ser Phe Ala Val Gly Asn Ala Ala Tyr Gln Ala Gly Pro
 1175 1180 1185
 5 Leu Gly Pro Ala Leu Ala Ala Ala Val Pro Ser Met Thr Gln Leu
 1190 1195 1200
 Leu Gly Asp Pro Gln Ala Gly Ile Arg Arg Asn Val Ala Ser Ala
 1205 1210 1215
 10 Leu Gly Asn Leu Gly Pro Glu Gly Leu Gly Glu Glu Leu Leu Gln
 1220 1225 1230
 Cys Glu Val Pro Gln Arg Leu Leu Glu Met Ala Cys Gly Asp Pro
 1235 1240 1245
 Gln Pro Asn Val Lys Glu Ala Ala Leu Ile Ala Leu Arg Ser Leu
 1250 1255 1260
 15 Gln Gln Glu Pro Gly Ile His Gln Val Leu Val Ser Leu Gly Ala
 1265 1270 1275
 Ser Glu Lys Leu Ser Leu Leu Ser Leu Gly Asn Gln Ser Leu Pro
 1280 1285 1290
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	Leu	Ala	Leu	Ser	Ala	Gln	Ser	Cys	Gly	Pro	Gly	Arg	Gly	Pro	Val	20	25	30	
10	Gly	Arg	Arg	Arg	Tyr	Val	Arg	Lys	Gln	Leu	Val	Pro	Leu	Leu	Tyr	35	40	45	
	Lys	Gln	Phe	Val	Pro	Ser	Met	Pro	Glu	Arg	Thr	Leu	Gly	Ala	Ser	50	55	60	
	Gly	Pro	Ala	Glu	Gly	Arg	Val	Thr	Arg	Gly	Ser	Glu	Arg	Phe	Arg	65	70	75	
15	Asp	Leu	Val	Pro	Asn	Tyr	Asn	Pro	Asp	Ile	Ile	Phe	Lys	Asp	Glu	80	85	90	
	Glu	Asn	Ser	Gly	Ala	Asp	Arg	Leu	Met	Thr	Glu	Arg	Cys	Lys	Glu	95	100	105	
20	Arg	Val	Asn	Ala	Leu	Ala	Ile	Ala	Val	Met	Asn	Met	Trp	Pro	Gly	110	115	120	
	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	125	130	135	
	Ala	Gln	Asp	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Leu	Asp	Ile	Thr	140	145	150	
25	Thr	Ser	Asp	Arg	Asp	Arg	Asn	Lys	Tyr	Gly	Leu	Leu	Ala	Arg	Leu	155	160	165	
	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Arg	Asn	170	175	180	
30	His	Ile	His	Val	Ser	Val	Lys	Ala	Asp	Asn	Ser	Leu	Ala	Val	Arg	185	190	195	
	Ala	Gly	Gly	Cys	Phe	Pro	Gly	Asn	Ala	Thr	Val	Arg	Leu	Arg	Ser	200	205	210	
	Gly	Glu	Arg	Lys	Gly	Leu	Arg	Glu	Leu	His	Arg	Gly	Asp	Trp	Val	215	220	225	
35	Leu	Ala	Ala	Asp	Ala	Ala	Gly	Arg	Val	Val	Pro	Thr	Pro	Val	Leu	230	235	240	
	Leu	Phe	Leu	Asp	Arg	Asp	Leu	Gln	Arg	Arg	Ala	Ser	Phe	Val	Ala	245	250	255	

Val Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp
 260 265 270
 His Leu Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp
 275 280 285
 5 Phe Ala Pro Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val
 290 295 300
 Leu Ala Pro Gly Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg
 305 310 315
 10 Val Ala Arg Glu Glu Ala Val Gly Val Phe Ala Pro Leu Thr Ala
 320 325 330
 His Gly Thr Leu Leu Val Asn Asp Val Leu Ala Ser Cys Tyr Ala
 335 340 345
 Val Leu Glu Ser His Gln Trp Ala His Arg Ala Phe Ala Pro Leu
 350 355 360
 15 Arg Leu Leu His Ala Leu Gly Ala Leu Leu Pro Gly Gly Ala Val
 365 370 375
 Gln Pro Thr Gly Met His Trp Tyr Ser Arg Leu Leu Tyr Arg Leu
 380 385 390
 20 Ala Glu Glu Leu Met Gly
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 30 Phe Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr
 35 40 45
 Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser
 50 55 60
 35 Gly Arg Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys
 65 70 75
 Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu
 80 85 90
 Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp
 95 100 105

	Lys	Leu	Asn	Ala	Leu	Ala	Ile	Ser	Val	Met	Asn	Gln	Trp	Pro	Gly	
					110					115					120	
	Val	Arg	Leu	Arg	Val	Thr	Glu	Gly	Trp	Asp	Glu	Asp	Gly	His	His	
					125					130					135	
5	Ser	Glu	Glu	Ser	Leu	His	Tyr	Glu	Gly	Arg	Ala	Val	Asp	Ile	Thr	
					140					145					150	
	Thr	Ser	Asp	Arg	Asp	Arg	Ser	Lys	Tyr	Gly	Met	Leu	Ala	Arg	Leu	
					155					160					165	
10	Ala	Val	Glu	Ala	Gly	Phe	Asp	Trp	Val	Tyr	Tyr	Glu	Ser	Lys	Ala	
					170					175					180	
	His	Ile	His	Cys	Ser	Val	Lys	Ala	Glu	Asn	Ser	Val	Ala	Ala	Lys	
					185					190					195	
	Ser	Gly	Gly	Cys	Phe	Pro	Gly	Ser	Ala	Thr	Val	His	Leu	Glu	Gln	
					200					205					210	
15	Gly	Gly	Thr	Lys	Leu	Val	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Arg	Val	
					215					220					225	
	Leu	Ala	Ala	Asp	Asp	Gln	Gly	Arg	Leu	Leu	Tyr	Ser	Asp	Phe	Leu	
					230					235					240	
20	Thr	Phe	Leu	Asp	Arg	Asp	Glu	Gly	Ala	Lys	Lys	Val	Phe	Tyr	Val	
					245					250					255	
	Ile	Glu	Thr	Leu	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	
					260					265					270	
	His	Leu	Leu	Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Gly	Pro	Thr	Pro	
					275					280					285	
25	Gly	Pro	Ser	Ala	Leu	Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	
					290					295					300	
	Val	Tyr	Val	Val	Ala	Glu	Arg	Gly	Gly	Asp	Arg	Arg	Leu	Leu	Pro	
					305					310					315	
30	Ala	Ala	Val	His	Ser	Val	Thr	Leu	Arg	Glu	Glu	Glu	Ala	Gly	Ala	
					320					325					330	
	Tyr	Ala	Pro	Leu	Thr	Ala	His	Gly	Thr	Ile	Leu	Ile	Asn	Arg	Val	
					335					340					345	
	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu	Glu	His	Ser	Trp	Ala	His	
					350					355					360	
35	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	Ala	His	Ala	Leu	Leu	Ala	Ala	
					365					370					375	
	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Gly	Gly	Gly	Gly	Gly	Ser	Ile	Pro	
					380					385					390	

Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly Ala Glu Pro Thr Ala
395 400 405

Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His Ile Gly Thr Trp
410 415 420

5 Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met Ala Val Lys
425 430 435

Ala Ser
437

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20 Arg Gly Ala Ala Leu Ser Gly Asn Val Thr Gly Pro Gly Pro Arg
35 40 45

Ser Ala Gly Gly Ser Ala Arg Arg Asn Ala Pro Val Thr Ser Pro
50 55 60

25 Pro Pro Pro Leu Leu Ser His Cys Gly Arg Ala Ala His Cys Glu
65 70 75

Pro Leu Arg Tyr Asn Val Cys Leu Gly Ser Ala Leu Pro Tyr Gly
80 85 90

Ala Thr Thr Thr Leu Leu Ala Gly Asp Ser Asp Ser Gln Glu Glu
95 100 105

30 Ala His Ser Lys Leu Val Leu Trp Ser Gly Leu Arg Asn Ala Pro
110 115 120

Arg Cys Trp Ala Val Ile Gln Pro Leu Leu Cys Ala Val Tyr Met
125 130 135

35 Pro Lys Cys Glu Asn Asp Arg Val Glu Leu Pro Ser Arg Thr Leu
140 145 150

Cys Gln Ala Thr Arg Gly Pro Cys Ala Ile Val Glu Arg Glu Arg
155 160 165

Gly Trp Pro Asp Phe Leu Arg Cys Thr Pro Asp His Phe Pro Glu
170 175 180

	Gly Cys Pro Asn Glu Val Gln Asn Ile Lys Phe Asn Ser Ser Gly	185	190	195
	Gln Cys Glu Ala Pro Leu Val Arg Thr Asp Asn Pro Lys Ser Trp	200	205	210
5	Tyr Glu Asp Val Glu Gly Cys Gly Ile Gln Cys Gln Asn Pro Leu	215	220	225
	Phe Thr Glu Ala Glu His Gln Asp Met His Ser Tyr Ile Ala Ala	230	235	240
10	Phe Gly Ala Val Thr Gly Leu Cys Thr Leu Phe Thr Leu Ala Thr	245	250	255
	Phe Val Ala Asp Trp Arg Asn Ser Asn Arg Tyr Pro Ala Val Ile	260	265	270
	Leu Phe Tyr Val Asn Ala Cys Phe Phe Val Gly Ser Ile Gly Trp	275	280	285
15	Leu Ala Gln Phe Met Asp Gly Ala Arg Arg Glu Ile Val Cys Arg	290	295	300
	Ala Asp Gly Thr Met Arg Phe Gly Glu Pro Thr Ser Ser Glu Thr	305	310	315
20	Leu Ser Cys Val Ile Ile Phe Val Ile Val Tyr Tyr Ala Leu Met	320	325	330
	Ala Gly Val Val Trp Phe Val Val Leu Thr Tyr Ala Trp His Thr	335	340	345
	Ser Phe Lys Ala Leu Gly Thr Thr Tyr Gln Pro Leu Ser Gly Lys	350	355	360
25	Thr Ser Tyr Phe His Leu Leu Thr Trp Ser Leu Pro Phe Val Leu	365	370	375
	Thr Val Ala Ile Leu Ala Val Ala Gln Val Asp Gly Asp Ser Val	380	385	390
30	Ser Gly Ile Cys Phe Val Gly Tyr Lys Asn Tyr Arg Tyr Arg Ala	395	400	405
	Gly Phe Val Leu Ala Pro Ile Gly Leu Val Leu Ile Val Gly Gly	410	415	420
	Tyr Phe Leu Ile Arg Gly Val Met Thr Leu Phe Ser Ile Lys Ser	425	430	435
35	Asn His Pro Gly Leu Leu Ser Glu Lys Ala Ala Ser Lys Ile Asn	440	445	450
	Glu Thr Met Leu Arg Leu Gly Ile Phe Gly Phe Leu Ala Phe Gly	455	460	465

	Phe Val Leu Ile Thr Phe Ser Cys His Phe Tyr Asp Phe Phe Asn	470	475	480
	Gln Ala Glu Trp Glu Arg Ser Phe Arg Asp Tyr Val Leu Cys Gln	485	490	495
5	Ala Asn Val Thr Ile Gly Leu Pro Thr Lys Lys Pro Ile Pro Asp	500	505	510
	Cys Glu Ile Lys Asn Arg Pro Ser Leu Leu Val Glu Lys Ile Asn	515	520	525
10	Leu Phe Ala Met Phe Gly Thr Gly Ile Ala Met Ser Thr Trp Val	530	535	540
	Trp Thr Lys Ala Thr Leu Leu Ile Trp Arg Arg Thr Trp Cys Arg	545	550	555
	Leu Thr Gly His Ser Asp Asp Glu Pro Lys Arg Ile Lys Lys Ser	560	565	570
15	Lys Met Ile Ala Lys Ala Phe Ser Lys Arg Arg Glu Leu Leu Gln	575	580	585
	Asn Pro Gly Gln Glu Leu Ser Phe Ser Met His Thr Val Ser His	590	595	600
20	Asp Gly Pro Val Ala Gly Ile Ala Phe Glu Leu Asn Glu Pro Ser	605	610	615
	Ala Asp Val Ser Ser Ala Trp Ala Gln His Val Thr Lys Met Val	620	625	630
	Ala Arg Arg Gly Ala Ile Leu Pro Gln Asp Val Ser Val Thr Pro	635	640	645
25	Val Ala Thr Pro Val Pro Pro Glu Glu Gln Ala Asn Leu Trp Leu	650	655	660
	Val Glu Ala Glu Ile Ser Pro Glu Leu Glu Lys Arg Leu Gly Arg	665	670	675
30	Lys Lys Lys Arg Arg Lys Arg Lys Lys Glu Val Cys Pro Leu Gly	680	685	690
	Pro Ala Pro Glu Leu His His Ser Ala Pro Val Pro Ala Thr Ser	695	700	705
	Ala Val Pro Arg Leu Pro Gln Leu Pro Arg Gln Lys Cys Leu Val	710	715	720
35	Ala Ala Asn Ala Trp Gly Thr Gly Glu Pro Cys Arg Gln Gly Ala	725	730	735
	Trp Thr Val Val Ser Asn Pro Phe Cys Pro Glu Pro Ser Pro His	740	745	750

Gln Asp Pro Phe Leu Pro Gly Ala Ser Ala Pro Arg Val Trp Ala
 755 760 765
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 155 160 165
 Gly Trp Pro Asp Phe Leu Arg Cys Thr Pro Asp His Phe Pro Glu
 170 175 180

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	Phe Thr Glu Ala Glu His Gln Asp Met His Ser Tyr Ile Ala Ala	230	235	240
10	Phe Gly Ala Val Thr Gly Leu Cys Thr Leu Phe Thr Leu Ala Thr	245	250	255
	Phe Val Ala Asp Trp Arg Asn Ser Asn Arg Tyr Pro Ala Val Ile	260	265	270
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15	Leu Ala Gln Phe Met Asp Gly Ala Arg Arg Glu Ile Val Cys Arg	290	295	300
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	Thr Val Ala Ile Leu Ala Val Ala Gln Val Asp Gly Asp Ser Val	380	385	390
30	Ser Gly Ile Cys Phe Val Gly Tyr Lys Asn Tyr Arg Tyr Arg Ala	395	400	405
	Gly Phe Val Leu Ala Pro Ile Gly Leu Val Leu Ile Val Gly Gly	410	415	420
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 Gln Cys Glu Ala Pro Leu Val Arg Thr Asp Asn Pro Lys Ser Trp
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	Phe Thr Glu Ala Glu His Gln Asp Met His Ser Tyr Ile Ala Ala	230	235	240
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	Phe Val Ala Asp Trp Arg Asn Ser Asn Arg Tyr Pro Ala Val Ile	260	265	270
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	Thr Ser Tyr Phe His Leu Leu Thr Trp Ser Leu Pro Phe Val Leu	365	370	375
	Thr Val Ala Ile Leu Ala Val Ala Gln Val Asp Gly Asp Ser Val	380	385	390
25	Ser Gly Ile Cys Phe Val Gly Tyr Lys Asn Tyr Arg Tyr Arg Ala	395	400	405
	Gly Phe Val Leu Ala Pro Ile Gly Leu Val Leu Ile Val Gly Gly	410	415	420
30	Tyr Phe Leu Ile Arg Gly Val Met Thr Leu Phe Ser Ile Lys Ser	425	430	435
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35	Phe Val Leu Ile Thr Phe Ser Cys His Phe Tyr Asp Phe Phe Asn	470	475	480
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10	Leu Thr Gly His Ser Asp Asp Glu Pro Lys Arg Ile Lys Lys Ser	560	565	570
	Lys Met Ile Ala Lys Ala Phe Ser Lys Arg Arg Glu Leu Leu Gln	575	580	585
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	Ala Asp Val Ser Ser Ala Trp Ala Gln His Val Thr Lys Met Val	620	625	630
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	Val Glu Ala Glu Ile Ser Pro Glu Leu Glu Lys Arg Leu Gly Arg	665	670	675
25	Lys Lys Lys Arg Arg Lys Arg Lys Lys Glu Val Cys Pro Leu Gly	680	685	690
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30	Ala Val Pro Arg Leu Pro Gln Leu Pro Arg Gln Lys Cys Leu Val	710	715	720
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	Trp Thr Val Val Ser Asn Pro Phe Cys Pro Glu Pro Ser Pro His	740	745	750
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	230	235	240
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	245	250	255
	Val Ala Leu Ser Ala Val Lys Pro Gly Asp Arg Val Leu Ala Met		
	260	265	270
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	275	280	285
	Asp Arg Glu Pro Asn Arg Leu Arg Ala Phe Gln Val Ile Glu Thr		
	290	295	300
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	365	370	375
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	380	385	390
	Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe		
	395	400	405
	Pro Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His		
	410	415	420
30	Trp Tyr Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu		
	425	430	435
	Glu Ser Thr Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser		
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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/07417

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/705 C12N1/19 C12N1/21 C12N5/10
C12N15/62 C07K19/00 C12N15/11 G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
----------	--	-----------------------

A	<p>TAKABATAKE T. ET AL.: "Hedgehog and patched gene expression in adult ocular tissues" FEBS LETTERS, vol. 410, 30 June 1997 (1997-06-30), pages 485-489, XP002101427 ISSN: 0014-5793 the whole document</p>	1-15
A	<p>MOTOYAMA J. ET AL.: "Ptch2, a second mouse Patched gene is co-expressed with Sonic hedgehog" NATURE GENETICS, vol. 18, February 1998 (1998-02), pages 104-106, XP002101696 ISSN: 1061-4036 cited in the application the whole document</p>	1-15

-/--

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier document but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search

19 July 1999

Date of mailing of the international search report

03/08/1999

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
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Fax: (+31-70) 340-3016

Authorized officer

Mandl, B

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/07417

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication where appropriate, of the relevant passages	Relevant to claim No.
A	WO 97 45541 A (LELAND S STANFORD JUNIOR - UNIVE ;UNIV CALIFORNIA (US)) 4 December 1997 (1997-12-04) the whole document ---	1-22, 26-28
E	WO 99 29854 A (ONTOGENY INC) 17 June 1999 (1999-06-17) the whole document ---	1-17, 19-21, 26-28
P,X	EP 0 879 888 A (SMITHKLINE BEECHAM PLC) 25 November 1998 (1998-11-25) the whole document ---	16-21,26
P,X	CARPENTER D. ET AL.: "Characterization of two patched receptors for the vertebrate hedgehog protein family" --- PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, vol. 95, no. 23, 10 November 1998 (1998-11-10), pages 13630-13634 13634, XP002101428 ISSN: 0027-8424 the whole document ---	1-17
P,X	ZAPHIROPOULOS P. G. ET AL.: "PTCH2, a novel human patched gene undergoing alternative splicing and up-regulated in basal cell carcinomas." CANCER RESEACH, vol. 59, 15 February 1999 (1999-02-15), pages 787-792, XP002109560 the whole document -----	1-15

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 99/07417

Box I Observations where certain claims were found uns archable (Continuation f item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 22-25
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees w re accompanied by the applicant's protest.
- ☐ No prot st accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 22-25

Present claims 19-25 relate to a compound defined by reference to a desirable characteristic or property, namely its antagonistic or agonistic effect on 'patched-2', respectively.

The claims cover all compounds having this characteristic or property, whereas the application provides support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for only a very limited number of such compounds. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible. Independent of the above reasoning, the claims also lack clarity (Article 6 PCT). An attempt is made to define the compound by reference to a result to be achieved. Again, this lack of clarity in the present case is such as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search has been carried out for those parts of the claims which appear to be clear, supported and disclosed, namely those parts relating to antisense oligonucleotides which can be obtained from the specific sequence as it is presented by SEQ.ID.1 by using general methods known to the person skilled in the art. Consequently, claims 19 and 20 were searched partially and claim 21 was searched completely.

Moreover, there is an inconsistency between claim 21 referring to an 'antisense nucleotide' and page 9, line 1, referring to an 'antisense oligonucleotide'. Due to the fact that only the term 'antisense oligonucleotide' makes sense in the context of claim 21, claim 21 was read as referring to an 'antisense oligonucleotide'.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 99/07417

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9745541 A	04-12-1997	AU 3227497 A	05-01-1998
WO 9929854 A	17-06-1999	NONE	
EP 0879888 A	25-11-1998	CA 2232808 A	23-11-1998
		JP 11075874 A	23-03-1999